IMPROVED ALPHAVIRUS REPLICONS AND HELPER CONSTRUCTS

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RELATED APPLICATIONS

The present application claims the benefit, under 35 U.S.C. § 119(e), of U.S. provisional application serial number 60/456,196, filed March 20, 2003, the entire contents of which are incorporated by reference herein in their entirety.

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FIELD OF THE INVENTION

The present invention relates to improved constructs for and methods of making recombinant alphavirus particles.

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BACKGROUND OF THE INVENTION

In eukaryotes, two distinct mechanisms have evolved in cells to initiate translation. In one of them, the methyl-7-guanosine (5′)pppN structure present at the 5′ end of the mRNA (the "cap") is recognized by the initiation factor eIF4F, which is

20 composed of eIF4E, eIF4G and eIF4A. The formation of this "pre-initiation complex" requires, among other factors, the concerted action of initiation factor eIF2, responsible for binding to the initiator tRNA-Met$_i$, and eIF3, which interacts with the 40S ribosomal subunit (Hershey & Merrick. *Translational Control of Gene Expression*, pp. 33–88, Cold Spring Harbor Laboratory Press, NY 2000).

25 In the alternative mechanism, translation initiation occurs internally on the transcript and is mediated by an internal ribosome entry sequence (IRES) element that recruits the translational machinery to an internal initiation codon in the mRNA with the help of *trans*-acting factors (Jackson. *Translational Control of Gene Expression*, pp. 127–184, Cold Spring Harbor Laboratory Press, NY 2000). IRES elements have

30 been found in numerous transcripts from viruses that infect vertebrate, invertebrate, or plant cells, as well as in transcripts from vertebrate and invertebrate genes.

During many viral infections, as well as in other cellular stress conditions, changes in the phosphorylation state of eIF2, which lower the levels of the ternary complex eIF2–GTP–tRNA-Met$_i$, result in overall inhibition of protein synthesis.

Conversely, specific shut-off of cap-dependent initiation depends upon modification of eIF4F functionality (Thompson & Sarnow. *Current Opinion in Microbiology* 3:366–370 (2000)).

IRES elements bypass cap-dependent translation inhibition; thus the translation directed by an IRES element is termed "cap-independent." IRES-driven translation initiation prevails during many viral infections, such as, for example, picornaviral infection (Macejak & Sarnow. *Nature* 353:90–94 (1991)). Under these circumstances, cap-dependent initiation is inhibited or severely compromised due to the presence of small amounts of functional eIF4F. This is caused by cleavage or loss of solubility of eIF4G (Gradi et al. *Proceedings of the National Academy of Sciences*, USA 95:11089–11094 (1998)); 4E-BP dephosphorylation (Gingras et al. *Proceedings of the National Academy of Sciences*, USA 93:5578–5583 (1996)) or poly(A)-binding protein (PABP) cleavage (Joachims et al. *Journal of Virology* 73:718–727 (1999)).

Alphavirus vectors that express a nucleic acid of interest (NOI) at varying levels have been described. All of these examples describe modification of the alphavirus non-structural protein genes or of the 26S (subgenomic) promoter to regulate vector replication or transcription from the subgenomic promoter. Examples include mutations in the non-structural protein genes that increase or decrease subgenomic RNA transcription or alter genomic RNA replication, resulting in modified NOI expression. Control of protein expression from an alphavirus vector, at the level of translation of the subgenomic mRNA, has not been described previously.

The present invention provides alphavirus replicon and helper vectors engineered to control the expression of one or more heterologous nucleic acid sequences at the level of protein translation via a cap-independent mechanism under the direction of an IRES element.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a recombinant replicon nucleic acid comprising: a first nucleic acid sequence encoding a 5' alphavirus replication recognition sequence, at least one second nucleic acid sequence encoding an alphavirus nonstructural protein, at least one alphavirus subgenomic promoter, at least one IRES element, at least one heterologous nucleic acid, and a third nucleic

acid encoding a 3' alphavirus replication recognition sequence, and an alphavirus packaging signal which allows the replicon to be packaged into particles.

In another embodiment, the present invention provides a recombinant helper nucleic acid comprising: a first nucleic acid sequence encoding a 5' alphavirus replication recognition sequence, an alphavirus subgenomic promoter, an IRES element, a nucleic acid encoding one or more than one alphavirus structural protein, and a third nucleic acid encoding a 3' alphavirus replication recognition sequence.

Also provided herein is an alphavirus particle comprising an alphavirus replicon RNA comprising the recombinant replicon nucleic acid of this invention. In a further embodiment, provided herein is a population of infectious, defective, alphavirus particles, wherein each particle contains an alphavirus replicon RNA comprising a recombinant replicon nucleic acid of this invention. In some embodiments, the invention provides a population of infectious, defective alphavirus particles wherein each particle contains an alphavirus replicon RNA comprising a recombinant replicon nucleic acid of this invention, and the population has no detectable replication-competent virus, as measured by passage on cell culture. In specific embodiments, the particles of this invention can contain one or more attenuating mutations.

In addition, pharmaceutical compositions are included, which comprise the particles and populations of this invention in a pharmaceutically acceptable carrier.

In other embodiments, the present invention provides a method of making infectious, defective alphavirus particles, comprising: (a) introducing into a population of cells (i) a recombinant replicon nucleic acid of this invention; and (ii) one or more helper nucleic acid(s) encoding alphavirus structural proteins; wherein all of the alphavirus structural proteins are provided in the cells; and (b) producing said alphavirus particles in the population of cells. The method of this invention can further comprise the step of collecting said alphavirus particles from the cells.

In some embodiments, the helper nucleic acid of this invention can also be a recombinant replicon nucleic acid of this invention. For example, a recombinant

nucleic acid of this invention can comprise, as a heterologous nucleic acid and/or in addition to a heterologous nucleic acid, a nucleic acid sequence encoding one alphavirus structural protein or more than one alphavirus structural protein. In such embodiments, the recombinant replicon nucleic acid is considered to be a recombinant

5   replicon helper nucleic acid, which can be present in a cell with other helper nucleic acids and/or other recombinant nucleic acids of this invention.

Thus, in a specific embodiment, the recombinant replicon nucleic acid of this invention further encodes an alphavirus structural protein or more than one alphavirus

10   structural protein. This recombinant replicon nucleic acid can be introduced into a population of cells together with one or more helper nucleic acids, such that the recombinant replicon nucleic acid and the helper nucleic acid(s) produce all of the alphavirus structural proteins, and the recombinant replicon nucleic acid is packaged into particles in said cells.

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Additionally provided are methods of eliciting an immune response in a subject, comprising administering to the subject an immunogenic amount of the nucleic acids, vectors, particles populations and/or compositions of this invention.

20   In further embodiments, the present invention provides a recombinant nucleic acid comprising: a promoter that directs transcription of a nucleic acid; an IRES element; and a nucleic acid comprising a coding sequence, wherein the IRES element is operably located such that translation of the coding sequence is via a cap-independent mechanism directed by the IRES element and not via a cap-dependent

25   mechanism.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a northern blot of spacer-IRES replicon subgenomic RNAs.

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DETAILED DESCRIPTION OF THE INVENTION

As used herein, "a," "an" and "the" can mean one or more than one, depending on the context in which it is used. As examples, "a cell" can mean one cell

5   or multiple cells; and "a heterologous nucleic acid" can mean one heterologous nucleic acid or multiple heterologous nucleic acids.

The present invention is based on the surprising and unexpected discovery that transcription of a nucleic acid and translation of the nucleic acid can be uncoupled.

10   Thus, in one embodiment, the present invention provides a recombinant nucleic acid comprising: a promoter that directs transcription; an IRES element; and a coding sequence, wherein the IRES element is operably located such that translation of the coding sequence is via a cap-independent mechanism directed by the IRES element and not via a cap-dependent mechanism. For the purposes of this invention, the term

15   "transcription" includes the production of RNA from an alphavirus subgenomic promoter of a recombinant replicon nucleic acid, which can itself be an RNA molecule. That is, the subgenomic promoter on a recombinant replicon RNA molecule of this invention can direct the transcription of a messenger RNA encoding a heterologous NOI. Separately, the recombinant replicon nucleic acid can be

20   "replicated," i.e., copied from the 5' replication recognition sequence through to the replication recognition sequence.

In other embodiments, the present invention provides a recombinant replicon nucleic acid comprising: a first nucleic acid sequence encoding a 5' alphavirus

25   replication recognition sequence, at least one second nucleic acid sequence encoding an alphavirus nonstructural protein, at least one alphavirus subgenomic promoter, at least one IRES element, at least one heterologous nucleic acid, and a third nucleic acid encoding a 3' alphavirus replication recognition sequence. In certain embodiments, the recombinant replicon nucleic acid further comprises an alphavirus

30   packaging signal so that the replicon can be packaged into particles. In further embodiments, the recombinant replicon nucleic acid can comprise a spacer nucleic acid sequence that can be located upstream of an IRES element.

It is understood that in various embodiments, the elements of the recombinant replicon nucleic acid of this invention can be present in the order listed herein and/or present in any order. Thus for example, in one embodiment, the present invention provides a recombinant replicon nucleic acid comprising, in the following order: a

5   first nucleic acid sequence encoding a 5' alphavirus replication recognition sequence, at least one second nucleic acid sequence encoding an alphavirus nonstructural protein, at least one alphavirus subgenomic promoter, at least one IRES element, at least one heterologous nucleic acid, and a third nucleic acid encoding a 3' alphavirus replication recognition sequence

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As used herein, a "5' alphavirus replication recognition sequence" and "3' alphavirus replication recognition sequence" are 5' and 3' sequences (the 5' and 3' designations referring to their location in the alphavirus nucleic acid), which control replication of an alphavirus genome. In certain embodiments, either or both the 5' and

15   3' alphavirus replication recognition sequences can be truncated at either end, provided that their function in replication of an alphavirus genome remains intact.

Also as used herein, "at least one second nucleic acid sequence encoding an alphavirus nonstructural protein" includes a nucleic acid sequence that encodes at

20   least one, and possibly more than one, alphavirus nonstructural protein. For example, a second nucleic acid sequence of this invention can be a contiguous nucleotide sequence encoding alphavirus nonstructural proteins nsp1, nsp2, nsp3 and nsp4, a contiguous nucleotide sequence encoding alphavirus nonstructural proteins nsp1, nsp2 and nsp3, a contiguous nucleic acid encoding alphavirus nonstructural proteins nsp2,

25   nsp3 and nsp4, a contiguous nucleic acid encoding alphavirus nonstructural proteins nsp1 and nsp2, a contiguous nucleic acid encoding alphavirus nonstructural proteins nsp3 and nsp 4, a contiguous nucleic acid encoding alphavirus nonstructural proteins nsp2 and nsp3, a nucleic acid encoding alphavirus nonstructural protein nsp1, a nucleic acid encoding alphavirus nonstructural protein nsp2, a nucleic acid encoding

30   alphavirus nonstructural protein nsp3, a nucleic acid encoding alphavirus nonstructural protein nsp4 and/or any combination and/or order thereof, such that the recombinant replicon nucleic acid comprises nucleotide sequences encoding nsp1, nsp2, nsp3 and nsp4 in total.

In particular embodiments, the recombinant replicon nucleic acid of this invention can comprise nucleic acid encoding one or more alphavirus nonstructural proteins in any combination and in any location relative to one another, such that the recombinant replicon nucleic acid comprises nucleotide sequences encoding nsp1,

5   nsp2, nsp3 and nsp4 in total. For example, a recombinant replicon nucleic acid of this invention can comprise, in the following order: a first nucleic acid sequence encoding a 5' alphavirus replication recognition sequence, a second nucleic acid sequence encoding alphavirus nonstructural protein nsp1, nsp2 and nsp3, at least one alphavirus subgenomic promoter, at least one IRES element, at least one heterologous nucleic

10   acid, another second nucleic acid sequence encoding alphavirus nonstructural protein nsp4, and a third nucleic acid encoding a 3' alphavirus replication recognition sequence

As also used herein, an "alphavirus subgenomic promoter," "subgenomic

15   promoter," or "26S promoter" is a promoter present in an alphavirus genome that directs transcription of a subgenomic message in a normal alphavirus replication process. The alphavirus subgenomic promoter can be truncated (e.g., to produce a minimal alphavirus subgenomic promoter) and/or modified such that its activity is reduced, maintained or increased, according to methods known in the art.

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The recombinant nucleic acids of this invention can comprise an internal ribosome entry sequence (IRES) element, which directs translation of a nucleic acid into a protein via a cap-independent mechanism, as described herein and as is well known in the art. In particular in the recombinant replicon nucleic acids of the present

25   invention, control of nucleic acid expression at the level of translation is accomplished by introducing an internal ribosome entry site (IRES) downstream of a alphavirus 26S subgenomic promoter and upstream of the coding sequence to be translated. The IRES element is positioned so that it directs translation of the mRNA, thereby minimizing, limiting or preventing initiation of translation of the mRNA from

30   the methyl-7-guanosine (5')pppN structure present at the 5' end of the subgenomic mRNA (the "cap"). This "IRES-directed," cap-independent translation does not require or result in any significant modification of alphavirus non-structural protein genes that could alter replication and transcription.

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Alphavirus vectors designed to control the expression level of a heterologous nucleic acid without modulating (e.g., disturbing, upsetting, perturbing, disrupting, increasing, enhancing, reducing, minimizing) genome replication or subgenomic transcription have several advantages over earlier vector designs. First, modulating

5   genome replication can negatively affect VRP generation by limiting the number of genomic RNAs available for packaging into particles. Second, modulating subgenomic transcription by altering (e.g., by truncation, deletion, addition and/or substitution) the 26S promoter can alter genomic RNA replication, again resulting in limiting the number of genomic RNAs available for packaging into particles. Third,

10 alphavirus replication induces a stress response in cells that can result in reduced cap-dependent translation of mRNAs. Switching from cap-dependent translation of an alphavirus subgenomic mRNA to the cap-independent mechanism provided by an IRES element minimizes this negative affect on NOI expression.

An IRES element of the present invention can include, but is not limited to,

15 viral IRES elements from picornaviruses, e.g., poliovirus (PV) or the human enterovirus 71, e.g. strains 7423/MS/87 and BrCr thereof; from encephalomyocarditis virus (EMCV); from foot-and-mouth disease virus (FMDV); from flaviviruses, e.g., hepatitis C virus (HCV); from pestiviruses, e.g., classical swine fever virus (CSFV); from retroviruses, e.g., murine leukemia virus (MLV); from lentiviruses, e.g., simian

20 immunodeficiency virus (SIV); from cellular mRNA IRES elements such as those from translation initiation factors, e.g., eIF4G or DAP5; from transcription factors, e.g., c-Myc (Yang and Sarnow, *Nucleic Acids Research* 25: 2800-2807 (1997)) or NF-κB-repressing factor (NRF); from growth factors, e.g., vascular endothelial growth factor (VEGF), fibroblast growth factor (FGF-2) and platelet-derived growth factor B

25 (PDGF B); from homeotic genes, e.g., *Antennapedia*; from survival proteins, e.g., X-linked inhibitor of apoptosis (XIAP) or Apaf-1; from chaperones, e.g., immunoglobulin heavy-chain binding protein BiP (Martínez-Salas et al., *Journal of General Virology* 82: 973-984, (2001)), from plant viruses, as well as any other IRES elements now known or later identified.

30 In certain embodiments, the IRES element of this invention can be derived from, for example, encephalomyocarditis virus (EMCV, GenBank accession # NC001479), cricket paralysis virus (GenBank accession # AF218039), Drosophila C

virus (GenBank accession # AF014388), *Plautia stali* intestine virus (GenBank accession # AB006531), *Rhopalosiphum padi* virus (GenBank accession # AF022937), Himetobi P virus (GenBank accession # AB017037), acute bee paralysis virus (GenBank accession # AF150629), Black queen cell virus (GenBank accession

5   # AF183905), Triatoma virus (GenBank accession # AF178440), *Acyrthosiphon pisum* virus (GenBank accession # AF024514), infectious flacherie virus (GenBank accession # AB000906), and/or Sacbrood virus (Genbank accession # AF092924). In addition, the present invention provides a synthetic IRES element, which can be designed, according to methods know in the art to mimic the function of naturally

10   occurring IRES elements (see Chappell et al. *Proc Natl Acad Sci U S A*. (2000) 97(4):1536-41.

In specific embodiments, the IRES element can be an insect IRES element or other non-mammalian IRES element that is functional in the particular helper cell line

15   chosen for packaging of the recombinant alphavirus particles of this invention, but would not be functional, or would be minimally functional, in a target host cell. Insect virus IRES elements have evolved to function optimally within insect cells and similarly mammalian-virus IRES sequences function optimally in mammalian cells. Thus, control of translation can be introduced into replicon vector systems by

20   inserting insect virus-specific IRES elements into replicon RNAs. In this way, translation of heterologous NOIs from replicon vectors can be regulated (attenuated) in mammalian cells and enhanced within insect cells. This is useful for those NOIs that are either toxic to the packaging cell or are detrimental to the alphavirus packaging process. An alternative way to achieve this effect is to use a mammalian

25   IRES element in the replicon vector that is packaged in an insect cell culture system, thereby also avoiding possibly significant translation of the heterologous NOI during packaging. Without being held to a particular hypothesis or theory, cellular factors and culture environment may play a role in IRES activity and function. Therefore, it is anticipated that additional levels of control/regulation of different IRES species

30   within the same cell may be achieved through the supply/removal of certain cellular factors or by changes in the culture environment (e.g., temperature) to preferentially direct translation to one IRES as compared to a second.

In some embodiments, the cellular environment of the helper or packaging cell line can be altered so that a specific activity of the IRES is either enhanced or reduced. Typically, IRES elements have evolved to function under conditions of cellular stress where increased levels of eIF-2alpha kinases result in reduced cap-dependent translation and a reciprocal increase in IRES-dependent translation/activity. Such conditions can be artificially induced in a cellular packaging system so as to increase expression from chosen IRES elements by a variety of methods including but not limited to hypoxia, hypothermia, nutritional/amino acid starvation, ER stress induction (e.g. using Thapsigargin), induction of interferon or PKR elements (e.g., using poly IC), blockage of tRNA dependent synthesis (e.g., using Edeine), or other general cell stressors known in the art, including but not limited to, hydrogen peroxide and sorbitol.

In other embodiments, IRES element-directed translation of the NOI can be modulated, e.g., through the use of anti-sense siRNAs specific for the IRES element/spacer or NOI which can be transfected into, or transduced/transiently expressed within the packaging cell by a number of standard methods known in the art and described herein.

As another alternative, the expression of the NOI can also be modulated by the use of ligand binding pairs, e.g., a nucleic acid element and a molecule (i.e. ligand) that binds to it (see, for example, U.S. Patent No. 6,242,259). Therefore, the present invention also provides a recombinant replicon nucleic acid comprising: a nucleic acid sequence encoding a 5' alphavirus replication recognition sequence, one or more second nucleic acid sequence(s) encoding an alphavirus nonstructural protein, at least one alphavirus subgenomic promoter, at least one IRES element, a non-alphavirus nucleotide sequence which, when bound by a ligand alters transcription of the subgenomic RNA and/or translation from the IRES, at least one heterologous nucleic acid, and a nucleic acid encoding a 3' alphavirus replication recognition sequence.

As a specific embodiment, the ligand can be an RNA binding protein (e.g., R17 coat protein), an antisense sequence, a dye (e.g., Hoechst dyes H33258 or H3342), and/or an antibiotic (e.g. tobramycin or kanamycin). These can be

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introduced into or produced in the packaging cells by methods known to those in the art (see U.S. Patent No. 6, 242, 259).

As utilized within the context of the present invention, a reduction of either transcription of subgenomic RNA, or a reduction of translation of a NOI directed by the IRES, due to the action of a ligand binding to a non-alphavirus nucleotide sequence located in close proximity to the alphavirus subgenomic promoter or IRES should be understood to refer to a statistically significant decrease of either transcription or translation, respectively, in the presence of the selected ligand. In some embodiments, the level of either transcription of subgenomic RNA or IRES-directed NOI translation in cells is reduced at least 25%, 50%, 75%, or 90%, or 3-fold, 5-fold, or 10-fold as compared to the levels without the presence of the binding ligand. A wide variety of assays that are known in the art can be utilized to assess a reduced level of transcription or translation, including for example, enzymatic assays of a reporter gene, northern blots, metabolic RNA labeling and the like.

The recombinant replicon nucleic acids of this invention can comprise one or more IRES elements and in those embodiments comprising two or more IRES elements, the IRES elements can be the same or they can be different, in any order and/or combination. In specific embodiments, the recombinant replicon nucleic acid can comprise two or more "promoter-IRES-heterologous NOI cassettes," in which the promoter, IRES and heterologous NOI in each cassette can be either different or the same. Alternatively, the recombinant replicon nucleic acid can encode two or more NOIs, one of which is controlled by a "promoter-IRES cassette," while the other NOI(s) can be controlled by a subgenomic promoter alone or by an IRES alone.

The heterologous nucleic acid of this invention is a nucleic acid that is not present in the genome of a wild type alphavirus and/or is not present in the genome of a wild type alphavirus in the same order as it exists in a recombinant replicon nucleic acid of this invention. For example, in certain embodiments, the heterologous nucleic acid of this invention can encode one or more alphavirus structural proteins (e.g., C, PE2/E2, E1, E3, 6K) and/or one or more alphavirus structural proteins in addition to a heterologous nucleic acid. When the recombinant replicon nucleic acid of this invention comprises nucleic acid encoding one or more alphavirus structural proteins,

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the recombinant replicon nucleic acid can function as a recombinant replicon helper nucleic acid in the assembly of infectious, defective alphavirus particles, as described herein.

5 The heterologous nucleic acid of this invention can encode a protein or peptide, which can be, but is not limited to, an antigen, an immunogen or immunogenic polypeptide or peptide, a fusion protein, a fusion peptide, a cancer antigen, etc. Examples of proteins and/or peptides encoded by the heterologous nucleic acid of this invention include, but are not limited to, immunogenic

10 polypeptides and peptides suitable for protecting a subject against a disease, including but not limited to microbial, bacterial, protozoal, parasitic, and viral diseases.

In some embodiments, for example, the protein or peptide encoded by the heterologous nucleic acid can be an orthomyxovirus immunogen (e.g., an influenza

15 virus protein or peptide such as the influenza virus hemagglutinin (HA) surface protein or the influenza virus nucleoprotein, or an equine influenza virus protein or peptide), or a parainfluenza virus immunogen, or a metapneumovirus immunogen, or a respiratory syncytial virus immunogen, or a rhinovirus immunogen, a lentivirus immunogen (e.g., an equine infectious anemia virus protein or peptide, a Simian

20 Immunodeficiency Virus (SIV) protein or peptide, or a Human Immunodeficiency Virus (HIV) protein or peptide, such as the HIV or SIV envelope GP160 protein, the HIV or SIV matrix/capsid proteins, and the HIV or SIV gag, pol and env gene products). The protein or peptide can also be an arenavirus immunogen (e.g., Lassa fever virus protein or peptide, such as the Lassa fever virus nucleocapsid protein and

25 the Lassa fever envelope glycoprotein), a picornavirus immunogen (e.g., a Foot and Mouth Disease virus protein or peptide), a poxvirus immunogen (e.g., a vaccinia protein or peptide, such as the vaccinia L1 or L8 protein), an orbivirus immunogen (e.g., an African horse sickness virus protein or peptide), a flavivirus immunogen (e.g., a yellow fever virus protein or peptide, a West Nile virus protein or peptide, or a

30 Japanese encephalitis virus protein or peptide), a filovirus immunogen (e.g., an Ebola virus protein or peptide, or a Marburg virus protein or peptide, such as NP and GP proteins), a bunyavirus immunogen (e.g., RVFV, CCHF, and SFS proteins or peptides), or a coronavirus immunogen (e.g., an infectious human coronavirus protein or peptide, such as the human coronavirus envelope glycoprotein, or a porcine

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transmissible gastroenteritis virus protein or peptide, or an avian infectious bronchitis virus protein or peptide). The protein or polypeptide encoded by the heterologous nucleic acid of this invention can further be a polio antigen, herpes antigen (e.g., CMV, EBV, HSV antigens) mumps antigen, measles antigen, rubella antigen, ,

5   varicella antigen, botulinum toxin, diphtheria toxin or other diphtheria antigen, pertussis antigen, hepatitis (e.g., Hepatitis A, Hepatitis B, Hepatitis C, Hepatitis D, or Hepatitis E) antigen, or any other vaccine antigen known in the art.

       As used herein, "eliciting an immune response" and "immunizing a subject"

10   includes the development, in a subject, of a humoral and/or a cellular immune response to a protein and/or polypeptide of this invention (e.g., an immunogen, an antigen, an immunogenic peptide, and/or one or more epitopes). A "humoral" immune response, as this term is well known in the art, refers to an immune response comprising antibodies, while a "cellular" immune response, as this term is well

15   known in the art, refers to an immune response comprising T-lymphocytes and other white blood cells, especially the immunogen-specific response by HLA-restricted cytolytic T-cells, i.e., "CTLs." A cellular immune response occurs when the processed immunogens, i.e., peptide fragments, are displayed in conjunction with the major histocompatibility complex (MHC) HLA proteins, which are of two general

20   types, class I and class II. Class I HLA-restricted CTLs generally bind 9-mer peptides and present those peptides on the cell surface. These peptide fragments in the context of the HLA Class I molecule are recognized by specific T-Cell Receptor (TCR) proteins on T-lymphocytes, resulting in the activation of the T-cell. The activation can result in a number of functional outcomes including, but not limited to expansion

25   of the specific T-cell subset resulting in destruction of the cell bearing the HLA-peptide complex directly through cytotoxic or apoptotic events or the activation of non-destructive mechanisms, e.g., the production of interferon/cytokines. Presentation of immunogens via Class I MHC proteins typically stimulates a CD8+ CTL response.

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       Another aspect of the cellular immune response involves the HLA Class II-restricted T-cell responses, involving the activation of helper T-cells, which stimulate and focus the activity of nonspecific effector cells against cells displaying the peptide fragments in association with the MHC molecules on their surface. At least two types

of helper cells are recognized: T-helper 1 cells (Th1), which secrete the cytokines interleukin 2 (IL-2) and interferon-gamma and T-helper 2 cells (Th2), which secrete the cytokines interleukin 4 (IL-4), interleukin 5 (IL-5), interleukin 6 (IL-6) and interleukin 10 (IL-10). Presentation of immunogens via Class II MHC proteins

5   typically elicits a CD4+ CTL response as well as stimulation of B lymphocytes, which leads to an antibody response.

An "immunogenic polypeptide," "immunogenic peptide," or "immunogen" as used herein includes any peptide, protein or polypeptide that elicits an immune

10   response in a subject and in certain embodiments, the immunogenic polypeptide is suitable for providing some degree of protection to a subject against a disease. These terms can be used interchangeably with the term "antigen."

In certain embodiments, the immunogen of this invention can comprise,

15   consist essentially of, or consist of one or more "epitopes." An "epitope" is a set of amino acid residues that is involved in recognition by a particular immunoglobulin. In the context of T cells, an epitope is defined as the set of amino acid residues necessary for recognition by T cell receptor proteins and/or MHC receptors. In an immune system setting, *in vivo* or *in vitro*, an epitope refers to the collective features of a

20   molecule, such as primary, secondary and/or tertiary peptide structure, and/or charge, that together form a site recognized by an immunoglobulin, T cell receptor and/or HLA molecule. In the case of a B-cell (antibody) epitope, it is typically a minimum of 3-4 amino acids, preferably at least 5, ranging up to approximately 50 amino acids. Preferably, the humoral response-inducing epitopes are between 5 and 30 amino

25   acids, usually between 12 and 25 amino acids, and most commonly between 15 and 20 amino acids. In the case of a T-cell epitope, an epitope includes at least about 7-9 amino acids, and for a helper T-cell epitope, at least about 12-20 amino acids. Typically, such a T-cell epitope will include between about 7 and 15 amino acids, e.g., 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids.

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The present invention can be employed to express a nucleic acid encoding an immunogenic polypeptide in a subject (*e.g.*, for vaccination) or for immunotherapy (*e.g.*, to treat a subject with cancer or tumors). Thus, in the case of vaccines, the present invention thereby provides methods of eliciting an immune response in a

subject, comprising administering to the subject an immunogenic amount of a nucleic acid, particle, population and/or composition of this invention.

It is also contemplated that the nucleic acids, particles, populations and pharmaceutical compositions of this invention can be employed in methods of delivering a NOI of interest to a cell, which can be a cell in a subject. Thus, the present invention provides a method of delivering a heterologous nucleic acid to a cell comprising introducing into a cell an effective amount of a nucleic acid, particle, population and/or composition of this invention. Also provided is a method of delivering a heterologous nucleic acid to a cell in a subject, comprising delivering to the subject an effective amount of a nucleic acid, particle, population and/or composition of this invention. Such methods can be employed to impart a therapeutic effect on a cell and/or a subject of this invention, according to well known protocols for gene therapy.

A "subject" of this invention includes, but is not limited to, warm-blooded animals, e.g., humans, non-human primates, horses, cows, cats, dogs, pigs, rats, and mice. Administration of the various compositions of this invention (e.g., nucleic acids, particles, populations, pharmaceutical compositions) can be accomplished by any of several different routes. In specific embodiments, the compositions can be administered intramuscularly, subcutaneously, intraperitoneally, intradermally, intranasally, intracranially, sublingually, intravaginally, intrarectally, orally, or topically. The compositions herein may be administered via a skin scarification method, or transdermally via a patch or liquid. The compositions can be delivered subdermally in the form of a biodegradable material that releases the compositions over a period of time.

The compositions of this invention can be used prophylactically to prevent disease or therapeutically to treat disease. Diseases that can be treated include infectious disease caused by viruses, bacteria, fungi or parasites, and cancer. Chronic diseases involving the expression of aberrant or abnormal proteins or the over-expression of normal proteins, can also be treated, e.g., Alzheimer's, disease multiple sclerosis, stroke, etc.

The compositions of this invention can be optimized and combined with other vaccination regimens to provide the broadest (i.e., all aspects of the immune response, including those features described hereinabove) cellular and humoral responses possible. In certain embodiments, this can include the use of heterologous prime-

5   boost strategies, in which the compositions of this invention are used in combination with a composition comprising one or more of the following: immunogens derived from a pathogen or tumor, recombinant immunogens, naked nucleic acids, nucleic acids formulated with lipid-containing moieties, non-alphavirus vectors (including but not limited to pox vectors, adenoviral vectors, herpes vectors, vesicular stomatitis

10   virus vectors, paramyxoviral vectors, parvovirus vectors, papovavirus vectors, retroviral vectors), and other alphavirus vectors. The viral vectors can be virus-like particles or nucleic acids. The alphavirus vectors can be replicon-containing particles, DNA-based replicon-containing vectors (sometimes referred to as an "ELVIS" system, see, for example, U.S. Patent No. 5,814,482) or naked RNA vectors.

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The compositions of the present invention can also be employed to produce an immune response against chronic or latent infectious agents, which typically persist because they fail to elicit a strong immune response in the subject. Illustrative latent or chronic infectious agents include, but are not limited to, hepatitis B, hepatitis C,

20   Epstein-Barr Virus, herpes viruses, human immunodeficiency virus, and human papilloma viruses. Alphavirus vectors encoding peptides and/or proteins from these infectious agents can be administered to a cell or a subject according to the methods described herein.

25   Alternatively, the immunogenic protein or peptide can be any tumor or cancer cell antigen. Preferably, the tumor or cancer antigen is expressed on the surface of the cancer cell. Exemplary cancer antigens for specific breast cancers are the HER2 and BRCA1 antigens. Other illustrative cancer and tumor cell antigens are described in S.A. Rosenberg, (1999) *Immunity* 10:281) and include, but are not limited to, MART-

30   1/MelanA, gp100, tyrosinase, TRP-1, TRP-2, MAGE-1, MAGE-3, GAGE-1/2, BAGE, RAGE, NY-ESO-1, CDK-4, β-catenin, MUM-1, Caspase-8, KIAA0205, HPVE&, SART-1, PRAME, p15 and p53 antigens, Wilms' tumor antigen, tyrosinase, carcinoembryonic antigen (CEA), prostate specific antigen (PSA), prostate-specific

membrane antigen (PSMA), prostate stem cell antigen (PSCA), human aspartyl (asparaginyl) β-hydroxylase (HAAH), and EphA2 (an epithelial cell tyrosine kinase, see International Patent Publication No. WO 01/12172).

5   The immunogenic polypeptide or peptide of this invention can also be a "universal" or "artificial" cancer or tumor cell antigen as described in international patent publication WO 99/51263, which is incorporated herein by reference in its entirety for the teachings of such antigens.

10   In various embodiments, the heterologous nucleic acid of this invention can encode an antisense nucleic acid sequence. An "antisense" nucleic acid is a nucleic acid molecule (i.e., DNA or RNA) that is complementary (*i.e.*, able to hybridize *in vivo* or under stringent *in vitro* conditions) to all or a portion of a nucleic acid (*e.g.*, a gene, a cDNA and/or mRNA) that encodes or is involved in the expression of nucleic

15   acid that encodes a polypeptide to be targeted for inhibited or reduced production by the action of the antisense nucleic acid. If desired, conventional methods can be used to produce an antisense nucleic acid that contains desirable modifications. For example, a phosphorothioate oligonucleotide can be used as the antisense nucleic acid to inhibit degradation of the antisense oligonucleotide by nucleases *in vivo*. Where the

20   antisense nucleic acid is complementary to a portion of the nucleic acid encoding the polypeptide to be targeted, the antisense nucleic acid should hybridize close enough to the 5' end of the nucleic acid encoding the polypeptide such that it inhibits translation of a functional polypeptide. Typically, this means that the antisense nucleic acid should be complementary to a sequence that is within the 5' half or third of the nucleic

25   acid to which it hybridizes.

An antisense nucleic acid of this invention can also encode a catalytic RNA (i.e., a ribozyme) that inhibits expression of a target nucleic acid in a cell by hydrolyzing an mRNA encoding the targeted gene product. Additionally,

30   hammerhead RNA can be used as an antisense nucleic acid to prevent intron splicing. An antisense nucleic acid of this invention can be produced and tested according to protocols routine in the art for antisense technology.

The term "alphavirus" as used herein has its conventional meaning in the art, and includes Eastern Equine Encephalitis virus (EEE), Venezuelan Equine Encephalitis virus (VEE), Everglades virus, Mucambo virus, Pixuna virus, Western Encephalitis virus (WEE), Sindbis virus, South African Arbovirus No. 86 (S.A.AR86), Girdwood S.A.

5   virus, Ockelbo virus, Semliki Forest virus, Middleburg virus, Chikungunya virus, O'Nyong-Nyong virus, Ross River virus, Barmah Forest virus, Getah virus, Sagiyama virus, Bebaru virus, Mayaro virus, Una virus, Aura virus, Whataroa virus, Babanki virus, Kyzlagach virus, Highlands J virus, Fort Morgan virus, Ndumu virus, Buggy Creek virus, and any other virus classified by the International Committee on Taxonomy of

10   Viruses (ICTV) as an alphavirus.

In specific embodiments of this invention, the nucleic acids and/or the proteins encoded by the nucleic acids of the present invention can comprise attenuating mutations. The phrases "attenuating mutation" and "attenuating amino acid," as used

15   herein, include a nucleotide sequence containing a mutation, or an amino acid encoded by a nucleotide sequence containing a mutation, which results in a decreased probability of causing disease in its host (i.e., reduction in or "attenuation of" virulence), in accordance with standard terminology in the art. See, e.g., Davis et al., MICROBIOLOGY 132 (3d ed. 1980). The phrase "attenuating mutation" excludes

20   mutations or combinations of mutations that would be lethal to the virus. However, it does include those otherwise lethal mutations that can be incorporated in combination with a resuscitating or rescuing mutation that leads to an attenuated phenotype.

Appropriate attenuating mutations will be dependent upon the alphavirus used,

25   and will be known to those skilled in the art. Exemplary attenuating mutations include, but are not limited to, those described in United States Patent No. 5,505,947 to Johnston et al., U.S. Patent No. 5,185,440 to Johnston et al., U.S. Patent No. 5,643,576 to Davis et al., U.S. Patent No. 5,792,462 to Johnston et al., and U.S. Patent No. 5,639,650 to Johnston et al., the disclosures of each of which are incorporated herein in their entireties

30   by reference.

In various embodiments of this invention, one or more of the alphavirus structural proteins of the alphavirus particles of this invention can comprise one or more attenuating mutations, for example, as defined in U.S. Patent Nos. 5,792,462

and 6,156,558. Specific attenuating mutations for the VEE E1 glycoprotein can include an attenuating mutation at any one of E1 amino acid positions 81, 272 and/or 253. Alphavirus particles made from the VEE-3042 mutant contain an isoleucine substitution at E1-81, and virus particles made from the VEE-3040 mutant contain an

5   attenuating mutation at E1-253. Specific attenuating mutations for the VEE E2 glycoprotein can include an attenuating mutation at any one of E2 amino acid positions 76, 120, or 209. Alphavirus particles made from the VEE-3014 mutant contain attenuating mutations at both E1-272 and at E2-209 (see U.S. Patent No. 5,792,492). A specific attenuating mutation for the VEE E3 glycoprotein includes an

10   attenuating mutation consisting of a deletion of E3 amino acids 56-59. Virus particles made from the VEE-3526 mutant contain this deletion in E3 (aa56-59) as well as a second attenuating mutation at E1-253. Specific attenuating mutations for the S.A.AR86 E2 glycoprotein include an attenuating mutation at any one of E2 amino acid positions 304, 314, 372, or 376. Alternatively, the attenuating mutation can be a

15   substitution, deletion and/or insertion of an amino acid in the E2 glycoprotein, for example, at any one or more of the following amino acid positions in any combination: 158, 159, 160, 161 and 162 (see Polo et al., PCT Publication No. WO 00/61772, the entire contents of which are incorporated by reference herein).

20   Another attenuating mutation of this invention can be an attenuating mutation at nucleotide 3 of the VEE genomic RNA, *i.e.*, the third nucleotide following the 5' methylated cap (*see, e.g.*, U.S. Patent No. 5,643,576, describing a G→C mutation at nt 3). The mutation can be a G→A, U or C, but can also be a G→A mutation in some embodiments.

25

When the alphavirus structural and/or non-structural proteins are from S.A.AR86, exemplary attenuating mutations in the structural and non-structural proteins include, but are not limited to, codons at nsp1 amino acid position 538 which specify an attenuating amino acid, preferably isoleucine as nsp1 amino acid 538; codons at E2

30   amino acid position 304 which specify an attenuating amino acid, preferably threonine as E2 amino acid 304; codons at E2 amino acid position 314 which specify an attenuating amino acid, preferably lysine as E2 amino acid 314; codons at E2 amino acid 372 which specify an attenuating amino acid, preferably leucine, at E2 amino acid residue 372; codons at E2 amino acid position 376 which specify an attenuating amino

acid, preferably alanine as E2 amino acid 376; in combination, codons at E2 amino acid residues 304, 314, 372 and 376 which specify attenuating amino acids, as described above; codons at nsp2 amino acid position 96 which specify an attenuating amino acid, preferably glycine as nsp2 amino acid 96; and codons at nsp2 amino acid position 372

5   which specify an attenuating amino acid, preferably valine as nsp2 amino acid 372; in combination, codons at nsp2 amino acid residues 96 and 372 which encode attenuating amino acids at nsp2 amino acid residues 96 and 372, as described above; codons at nsp2 amino acid residue 529 which specify an attenuating amino acid, preferably leucine, at nsp2 amino acid residue 529; codons at nsp2 amino acid residue 571 which specify an

10   attenuating amino acid, preferably asparagine, at nsp2 amino acid residue 571; codons at nsp2 amino acid residue 682 which specify an attenuating amino acid, preferably arginine, at nsp2 amino acid residue 682; codons at nsp2 amino acid residue 804 which specify an attenuating amino acid, preferably arginine, at nsp2 amino acid residue 804; codons at nsp3 amino acid residue 22 which specify an attenuating amino acid,

15   preferably arginine, at nsp3 amino acid residue 22; and in combination, codons at nsp2 amino acid residues 529, 571, 682 and 804 and at nsp3 amino acid residue 22 which specify attenuating amino acids, as described above.

20   Other illustrative attenuating mutations include those described in PCT Application No. PCT/US01/27644 (the disclosure of which is incorporated herein in its entirety by reference). For example, the attenuating mutation can be an attenuating mutation at amino acid position 537 of the S.A.AR86 nsp3 protein, more preferably a substitution mutation at this position, still more preferably a nonsense mutation that results in substitution of a termination codon. Translational termination (*i.e.*, stop)

25   codons are known in the art, and include the "opal" (UGA), "amber" (UAG) and "ochre" (UAA) termination codons. In embodiments of the invention, the attenuating mutation can result in a Cys→opal substitution at S.A.AR86 nsp3 amino acid position 537.

30   Further exemplary attenuating mutations can include an attenuating insertion mutation following amino acid 385 of the S.A.AR86 nsp3 protein. The insertion can comprise an insertion of at least 2, 4, 6, 8, 10, 12, 14, 16 or 20 amino acids. In some embodiments of the invention, the inserted amino acid sequence is rich in serine and

-threonine residues (e.g., comprises at least 2, 4, 6, or 8 such sites) that serve as a substrate for phosphorylation by serine/threonine kinases.

5   In certain embodiments, the attenuating mutation can comprise insertion of the amino acid sequence Ile-Thr-Ser-Met-Asp-Ser-Trp-Ser-Ser-Gly-Pro-Ser-Ser-Leu-Glu-Ile-Val-Asp (**SEQ ID NO:1**) following amino acid 385 of nsp3 (*i.e.*, the first amino acid is designated as amino acid 386 in nsp3). In other embodiments of the invention, the insertion mutation can comprise insertion of a fragment of **SEQ ID NO:1** that results in an attenuated phenotype. The fragment can comprise at least 4,

10   6, 8, 10, 12, 14, 15, 16 or 17 contiguous amino acids from **SEQ ID NO:1**.

        Those skilled in the art will appreciate that other attenuating insertion sequences comprising a fragment of the sequence set forth above, or which incorporate conservative amino acid substitutions into the sequence set forth above,

15   can be routinely identified by routine methods (as described above). While not wishing to be bound by any theory of the invention, it appears that the insertion sequence of **SEQ ID NO:1** is highly phosphorylated at serine residues, which confers an attenuated phenotype. Thus, other attenuating insertion sequences that serve as substrates for serine (or threonine) phosphorylation can be identified by conventional

20   techniques known in the art. Alternatively, or additionally, there is a Tyr→Ser substitution at amino acid 385 of the S.A.AR86 nsp3 protein *(i.e.,* just prior to the insertion sequence above). This sequence is conserved in the non-virulent Sindbis-group viruses, but is deleted from S.A.AR86

25   In other embodiments, the alphavirus of this invention can be any Sindbis virus strain (e.g., TR339), VEE (having a mutation at nucleotide 3 of the genomic RNA following the methylated cap), S.A.AR86 virus, Girdwood S.A. virus, Ockelbo virus, and/or chimeric viruses thereof. The complete genomic sequences, as well as the sequences of the various structural and non-structural proteins, are known in the art for

30   numerous alphaviruses and include: Sindbis virus genomic sequence (GenBank Accession No. J02363, NCBI Accession No. NC_001547), S.A.AR86 genomic sequence (GenBank Accession No. U38305), VEE genomic sequence (GenBank Accession No. L04653, NCBI Accession No. NC_001449), Girdwood S.A genomic sequence (GenBank Accession No. U38304), Semliki Forest virus genomic sequence

(GenBank Accession No. X04129, NCBI Accession No. NC_003215), and the TR339 genomic sequence (Klimstra et al. (1988) *J. Virol.* **72**:7357; McKnight et al.(1996) *J. Virol.* **70**:1981).

5   In particular embodiments of the present invention, the alphavirus structural protein of this invention can be a Sindbis virus structural protein, a SFV structural protein, a VEE structural protein, a Ross River virus structural protein, a S.A. AR86 structural protein, an EEE structural protein and/or a WEE structural protein. These can be present in any combination with one another and can be present in combination

10   with any alphavirus nonstructural proteins and/or other alphaviral sequences, such as the 5' alphavirus replication recognition sequence, the alphavirus subgenomic promoter and the 3' alphavirus replication recognition sequence, from any of these and/or other alphaviruses, to produce chimeric recombinant alphavirus particles and/or chimeric recombinant nucleic acids of this invention.

15

       In further embodiments, the IRES element of this invention directs the translation of the gene product encoded by the heterologous nucleic acid of the recombinant nucleic acid of this invention, such that at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 92%,

20   94%, 95%, 96%, 97%, 98%, 99% or 100% of the translation of the gene product encoded by the heterologous nucleic acid is controlled by the activity of the IRES element. The percentage of translation of the gene product encoded by the heterologous nucleic acid in the recombinant replicon nucleic acids of this invention as controlled by the IRES can be determined according to assays well known in the

25   art and as described in the Examples section provided herein.

       Furthermore, in embodiments of this invention wherein the IRES element of this invention directs the translation of an alphavirus structural protein present in a helper construct of this invention, the IRES element of this invention can direct the

30   translation of the structural protein(s), such that at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or 100% of the translation of the structural protein is controlled by the activity of the IRES element. The percentage of translation of the structural protein(s) as controlled by the IRES element of this invention can be

determined according to assays well known in the art and as described in the Examples section provided herein.

5

The nucleic acid of this invention can be RNA or DNA.

In another embodiment of this invention, a series of helper nucleic acids ("helper constructs" or "helper molecules"), i.e., recombinant DNA or RNA molecules that express one or more alphavirus structural proteins, are provided. In one set of RNA embodiments, the helper construct comprises a first nucleic acid

10 sequence encoding (i) a 5' alphavirus replication recognition sequence, (ii) a transcriptional promoter, (iii) a nucleic acid sequence encoding at least one, but not all, alphavirus structural proteins, and (iv) an alphavirus 3' replication recognition sequence. In certain embodiments, the E1 and E2 glycoproteins are encoded by one helper construct, and the capsid protein is encoded by another separate helper construct.

15 In another embodiment, the E1 glycoprotein, E2 glycoprotein, and capsid protein are each encoded by separate helper constructs. In other embodiments, the capsid protein and one of the glycoproteins are encoded by one helper construct, and the other glycoprotein is encoded by a separate second helper construct. In yet further embodiments, the capsid protein and glycoprotein E1 are encoded by one helper

20 construct and the capsid protein and glycoprotein E2 are encoded by a separate helper construct. In certain embodiments, the helper constructs of this invention do not include an alphavirus packaging signal.

Alternatively, the above-described helper nucleic acids are constructed as

25 DNA molecules, which can be stably integrated into the genome of a helper cell or expressed from an episome (e.g., an EBV derived episome). The DNA molecule can also be transiently expressed in a cell. The DNA molecule can be any vector known in the art, including but not limited to, a non-integrating DNA vector, such as a plasmid, or a viral vector. The DNA molecule can encode one or all of the alphavirus

30 structural proteins, in any combination, as described herein.

The helper constructs of this invention are introduced into "helper cells," which are used to produce the alphavirus particles of this invention. As noted above, the nucleic acids encoding alphavirus structural proteins can be present in the helper

cell transiently or by stable integration into the genome of the helper cell. The nucleic acid encoding the alphavirus structural proteins that are used to produce alphavirus particles of this invention can be under the control of constitutive and/or inducible promoters. As also noted above, the alpha virus structural protein coding sequences

5   can be provided on a recombinant replicon nucleic acid and/or a helper construct comprising an IRES element and the translation of these coding sequences can be controlled by the activity of an IRES element. In such embodiments, the IRES element can be active in the specific helper cell type and not active, or minimally active in other cells types. In particular embodiments, the helper cells of the invention

10   comprise nucleic acid sequences encoding the alphavirus structural proteins in a combination and/or amount sufficient to produce an alphavirus particle of this invention when a recombinant replicon nucleic acid is introduced into the cell under conditions whereby the alphavirus structural proteins are produced and the recombinant replicon nucleic acid is packaged into alphavirus particle of this

15   invention.

In all of the embodiments of this invention, it is contemplated that at least one of the alphavirus structural and/or non-structural proteins encoded by the recombinant replicon nucleic acid and/or helper molecules, and/or the nontranslated regions of the

20   recombinant replicon and/or helper nucleic acid, can contain one or more attenuating mutations in any combination, as described herein and as are well known in the literature.

In particular constructs of this invention, a promoter for directing transcription

25   of RNA from DNA, i.e., a DNA dependent RNA polymerase, is employed. In the RNA helper and replicon embodiments of this invention, the promoter is utilized to synthesize RNA in an *in vitro* transcription reaction, and specific promoters suitable for this use include, but are not limited to, the SP6, T7, and T3 RNA polymerase promoters. In the DNA helper embodiments, the promoter functions within a cell to

30   direct transcription of RNA. Potential promoters for *in vivo* transcription of the construct include, but are not limited to, eukaryotic promoters such as RNA polymerase II promoters, RNA polymerase III promoters, or viral promoters such as MMTV and MoSV LTR, SV40 early region, RSV or CMV. Many other suitable mammalian and viral promoters for the present invention are available and are known

24

in the art. Alternatively, DNA dependent RNA polymerase promoters from bacteria or bacteriophage, e.g., SP6, T7, and T3, can be employed for use *in vivo*, with the matching RNA polymerase being provided to the cell, either via a separate plasmid, RNA vector, or viral vector. In a specific embodiment, the matching RNA

5   polymerase can be stably transformed into a helper cell line under the control of an inducible promoter. Constructs that function within a cell can function as autonomous plasmids transfected into the cell and/or they can be stably transformed into the genome. In a stably transformed cell line, the promoter can be an inducible promoter, so that the cell will only produce the RNA polymerase encoded by the

10   stably transformed construct when the cell is exposed to the appropriate stimulus (inducer). The helper constructs are introduced into the stably transformed cell concomitantly with, prior to, and/or after exposure to, the inducer, thereby effecting expression of the alphavirus structural proteins. Alternatively, constructs designed to function within a cell can be introduced into the cell via a viral vector, such as, e.g.,

15   adenovirus, poxvirus, adeno-associated virus, SV40, retrovirus, nodavirus, picornavirus, vesicular stomatitis virus, and baculoviruses with mammalian pol II promoters.

In certain embodiments of the invention provided herein, the recombinant

20   replicon nucleic acid and/or helper nucleic acid of this invention can comprise a spacer nucleic acid, which can be located upstream of an IRES element in a recombinant replicon nucleic acid and/or helper nucleic acid of this invention. The spacer nucleic acid can comprise, consist essentially of, or consist of any random or specific non-coding nucleic acid sequence which is of a length sufficient to prevent at

25   least some, and in some embodiments, all translation from the 5' cap of a messenger RNA, such that translation is then directed by the IRES, in part or in whole. Alternatively, the spacer nucleic acid can be of a length and sequence structure that imparts sufficient secondary structure to the nucleic acid to prevent at least some and possibly all translation activity from the 5' cap of a messenger RNA.

30

As one example, a commercially available plasmid, pCDNA 3.1(-), was digested with a restriction enzyme, AluI, which cuts frequently within this plasmid, thus generating many random and differently sized fragments (see Example 3 for details). The pCDNA plasmid is 5427 nucleotides in length, and is a eukaryotic

expression vector, comprising various promoters (CMV, T7, SV40) for expression of an inserted nucleic acid as well as polyadenylation signals and antibiotic resistance genes. The AluI enzyme cuts throughout these elements, providing a range of random fragments. Examples of several different spacers and their sequences that were

5 generated from this example and which do not encode any functional elements from the plasmid, are provided hereinbelow:

357 nucleotide spacer:
CTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGC
10 AATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAG
CTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACC
AAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTC
TGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGC
TGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGT
15 TACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACA
GCCCAG

342 nucleotide spacer:
CTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAA
20 AAGCTTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGATCG
TTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGG
GTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTC
TGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGT
CAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGC
25 GGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAG

257 nucleotide spacer:
CTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAA
AGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTC
30 CACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTAT
CAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGG
GTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGAT
TTAGAG

35 383 nucleotide spacer:
CTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCG
TCCTGCAGTTCATTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAAC
CGGGCGCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCG
ATTGTCTGTTGTGCCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCC
40 GGAGAACCTGCGTGCAATCCATCTTGTTCAATCATGCGAAACGATCCTCAT
CCTGTCTCTTGATCAGATCCGAAAATGGATATACAAGCTCACTCATTAGGC
ACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGT
GAGCGGATAACAATTTCACACAGGAAACAG

579 nucleotide spacer:
CTGCAATAAACAAGTTGGGGTGGGCGAAGAACTCCAGCATGAGATCCCCG
CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAA
5   CCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGG
GCGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACT
CGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGAT
ACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTTGTATA
TCCATTTTCGGATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATT
10   GAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCT
ATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCG
TGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACC
TGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGG
CTGGCCACGACGGGCGTTCCTTGCGCAG

15

749 nucleotide spacer:
CTGCAATAAACAAGTTGGGGTGGGCGAAGAACTCCAGCATGAGATCCCCG
CGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAA
CCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGG
20   GCGTCGCTTGGTCGGTCATTTCGAACCCCAGAGTCCCGCTCAGAAGAACT
CGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGAT
ACCGTAAAGCACGAGGAAGCGGTCAGCCCATTCGCCGCCAAGCTCTTCAG
CAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCC
AGCCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGAT
25   ATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGG
GCATGCGCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGA
TGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTA
CGTGCTCGCTCGATGCGATGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCC
GGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTT
30   CTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCGGCACTTCGC
CCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAG

In addition to the use of random nucleic acid fragments generated from an

unrelated plasmid (as in the AluI fragments described above), it is also possible to use

35   fragments from cellular or viral genes, e.g., from the 5' non-coding regions of genes,

as spacers. One approach is to use the non-coding sequences surrounding an existing

IRES (see Example 4B.4.); another approach is to use the 5'non-coding region of an

alphaviral gene, e.g., the capsid gene (see Example 4A.2.)

40   Thus, it is contemplated that the spacer nucleic acid of this invention can be at

a minimum, at least 25 nucleic acids in length and can be as long as permissible in a

given recombinant replicon nucleic acid. For example, the spacer nucleic acid of this

invention can be, in certain embodiments, approximately 25, 30, 35, 40, 45, 50,55, 60,

65, 75, 80, 85, 90, 95, 100, 110, 115, 120, 125, 130, 135, 140, 145, 150, 160, 170,

175, 180, 190, 200, 210, 220, 225, 230, 235, 240, 245, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 50, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000,7500, 8000, 8500, 9000, 9500, or 10,000 nucleotides in length. By "approximately" it is meant that the spacer nucleic acid can vary up to 10%, 15%, 20% and/or 25% in length.

The spacer nucleic acid of this invention can also be a nucleotide sequence placed 3' to a 5' sequence for initiating transcription of a messenger RNA, and 5' to a functional IRES element, wherein the level of translation directed from said IRES element is at least approximately five fold higher than the level obtained from a non-functional IRES element. In preferred embodiments, the level of translation is at least approximately 10-fold, 20-fold, 50-fold, 100-fold, 150-fold, 180-fold, 200- fold, 300-fold, 400-fold or 500-fold higher. In other embodiments, at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, 99% or 100% of the translation of the gene product encoded by the heterologous nucleic acid and/or the structural protein(s) encoded by an IRES-containing helper construct is controlled by the activity of the IRES element.

The present invention also provides an alphavirus particle comprising a recombinant replicon nucleic acid of this invention. Also provided is a population of infectious, defective, alphavirus particles, wherein each particle contains an alphavirus replicon RNA comprising the recombinant replicon nucleic acid of this invention. In some embodiments, the population of this invention has no detectable replication-competent virus, as measured by passage on cell culture and/or other well known assays for detection of replication competent virus.

The present invention further provides a pharmaceutical composition comprising a nucleic acid, vector, particle and/or population of this invention in a pharmaceutically acceptable carrier. By "pharmaceutically acceptable" is meant a material that is not biologically or otherwise undesirable, i.e., the material may be administered to an individual along with the selected peptide, polypeptide, nucleic acid, vector or cell without causing substantial deleterious biological effects or interacting in a deleterious manner with any of the other components of the composition in which it is contained.

28

Furthermore, any of the compositions of this invention can comprise a pharmaceutically acceptable carrier and a suitable adjuvant. As used herein, "suitable adjuvant" describes an adjuvant capable of being combined with the peptide or
5   polypeptide of this invention to further enhance an immune response without deleterious effect on the subject or the cell of the subject. A suitable adjuvant can be, but is not limited to, MONTANIDE ISA51 (Seppic, Inc., Fairfield, NJ), SYNTEX adjuvant formulation 1 (SAF-1), composed of 5 percent (wt/vol) squalene (DASF, Parsippany, N.J.), 2.5 percent Pluronic, L121 polymer (Aldrich Chemical,
10   Milwaukee), and 0.2 percent polysorbate (Tween 80, Sigma) in phosphate-buffered saline. Other suitable adjuvants are well known in the art and include QS-21, Freund's adjuvant (complete and incomplete), aluminum salts (alum), aluminum phosphate, aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as
15   nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE) and RIBI, which contains three components extracted from bacteria, monophosphoryl lipid A, trealose dimycolate and cell wall skeleton (MPL+TDM+CWS) in 2% squalene/Tween 80 emulsion. Adjuvants can be
20   combined, either with the compositions of this invention or with other vaccine compositions that can be used in combination with the compositions of this invention. Examples of adjuvants can also include, but are not limited to, oil-in-water emulsion formulations, immunostimulating agents, such as bacterial cell wall components or synthetic molecules, or oligonucleotides (e.g. CpGs) and nucleic acid polymers (both
25   double stranded and single stranded RNA and DNA), which can incorporate alternative backbone moieties, e.g., polyvinyl polymers.

The compositions of the present invention can also include other medicinal agents, pharmaceutical agents, carriers, diluents, immunostimulatory cytokines, etc.
30   Actual methods of preparing such dosage forms are known, or will be apparent, to those skilled in this art. Preferred dosages for alphavirus replicon particles, as contemplated by this invention, can range from 10^3 to 10^{10} particles per dose. For humans, 10^6, 10^7 or 10^8 are preferred doses. A dosage regimen can be one or more doses hourly, daily, weekly, monthly, yearly, etc. as deemed necessary to achieve the

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desired prophylactic and./or therapeutic effect to be achieved by administration of a composition of this invention to a subject. The efficacy of a particular dosage can be determined according to methods well known in the art.

5   The present invention further provides a method of making infectious, defective alphavirus particles, comprising: a) introducing into a cell the following: (i) a recombinant replicon nucleic acid of this invention, and (ii) one or more helper nucleic acids encoding alphavirus structural proteins, wherein the one or more helper nucleic acids produce all of the alphavirus structural proteins, and b) producing said 10   alphavirus particles in the cell. In some embodiments, the recombinant replicon nucleic acid can comprise at least one heterologous nucleic acid encoding an alphavirus structural protein.

In other embodiments of the methods of this invention, the helper nucleic acid 15   can be a recombinant nucleic acid comprising a 5' alphavirus replication recognition sequence, an alphavirus subgenomic promoter, a nucleic acid encoding an alphavirus structural protein and a 3' alphavirus replication recognition sequence.

In further embodiments, the helper nucleic acid can be a recombinant nucleic 20   acid (which can be DNA) comprising a promoter (e.g., a CMV promoter) and nucleotide sequences encoding one or more, including all, alphavirus structural proteins.

The helper nucleic acid of this invention can comprise nucleic acid sequences 25   encoding any one or more of the alphavirus structural proteins (C, E1, E2) in any order and/or in any combination. Thus, a helper cell can comprise as many helper nucleic acids as needed in order to provide all of the alphavirus structural proteins necessary to produce alphavirus particles. A helper cell can also comprise helper nucleic acid(s) stably integrated into the genome of a helper (e.g., packaging) cell. In 30   such helper cells, the alphavirus structural proteins can be produced under the control of a promoter that can be an inducible promoter.

In some embodiments, the helper nucleic acid employed in the methods of this invention can be a recombinant nucleic acid comprising a 5' alphavirus replication

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recognition sequence, an IRES element, a nucleic acid encoding an alphavirus structural protein and a 3' alphavirus replication recognition sequence.

In further embodiments, the helper nucleic acid can be a recombinant nucleic 5 acid comprising a 5' alphavirus replication recognition sequence, an alphavirus subgenomic promoter, an IRES element, a nucleic acid encoding one or more alphavirus structural proteins and a 3' alphavirus replication recognition sequence.

Additionally provided herein is a method of making infectious, defective 10 alphavirus particles, comprising: a) introducing into a cell the following: i) an alphavirus replicon RNA comprising a 5' alphavirus replication recognition sequence, nucleic acid sequence(s)encoding alphavirus nonstructural proteins, an alphavirus subgenomic promoter, a heterologous nucleic acid sequence and a 3' alphavirus replication recognition sequence; and ii) one or more helper nucleic acids encoding 15 alphavirus structural proteins comprising a 5' alphavirus replication recognition sequence, an alphavirus subgenomic promoter, an IRES element, a nucleic acid encoding one or more alphavirus structural proteins and a 3' alphavirus replication recognition sequence, whereby all of the alphavirus structural proteins are produced in the cell; and b) producing said alphavirus particles in the cell.
20

A method is also provided herein of making infectious, defective alphavirus particles, comprising: a) introducing into a cell the following: i) an alphavirus replicon RNA comprising a 5' alphavirus replication recognition sequence, nucleic acid sequence(s) encoding alphavirus nonstructural proteins, at least one alphavirus 25 subgenomic promoter, at least one IRES element, at least one heterologous nucleic acid sequence and a 3' alphavirus replication recognition sequence; and ii) one or more helper nucleic acids encoding alphavirus structural proteins comprising a 5' alphavirus replication recognition sequence, an alphavirus subgenomic promoter, an IRES element, a nucleic acid encoding one or more alphavirus structural proteins and 30 a 3' alphavirus replication recognition sequence, whereby all of the alphavirus structural proteins are produced in the cell; and b) producing said alphavirus particles in the cell.

The methods of making alphavirus particles of this invention can further comprise the step of collecting said alphavirus particles from the cell.

The present invention also provides a recombinant nucleic acid comprising 5'
alphavirus replication recognition sequence, an alphavirus subgenomic promoter, an IRES element, a nucleic acid encoding one or more alphavirus structural proteins in any combination and/or order and a 3' alphavirus replication recognition sequence. In some embodiments, this recombinant helper nucleic acid can comprise a spacer nucleotide sequence that can be upstream of an IRES element. Also provided is a vector and/or a cell comprising this recombinant nucleic acid.

Additionally provided herein is recombinant nucleic acid comprising:
a first nucleic acid sequence encoding a 5' alphavirus replication recognition sequence; at least one second nucleic acid sequence encoding an alphavirus nonstructural protein; a first alphavirus subgenomic promoter; a first IRES element; a first heterologous nucleic acid; a second alphavirus subgenomic promoter; a second IRES element; a third nucleic acid encoding a 3' alphavirus replication recognition sequence. In some embodiments, the first and second alphavirus subgenomic promoter can be the same or different, the first and second IRES element can be the same or different and/or the first and second heterologous nucleic acid can be the same or different. This recombinant nucleic acid can comprise an alphavirus packaging signal and/or a spacer nucleotide sequence that can be upstream of an IRES element. This recombinant nucleic acid can also comprise one or more second nucleic acid sequences encoding alphavirus nonstructural proteins in any order and/or combination, such that all four of the alphavirus nonstructural protein coding sequences are present on the recombinant nucleic acid. This recombinant nucleic acid can be present in an alphavirus particle of this invention and such particles can be present as a population of this invention and/or in a pharmaceutical composition of this invention.

Also provided is a recombinant replicon nucleic acid as described above, further comprising a third or further additional alphavirus subgenomic promoter, a third or further additional IRES element and/or a third or further additional heterologous nucleic acid. This recombinant nucleic acid can be present in an

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alphavirus particle of this invention and such particles can be present as a population of this invention and/or in a pharmaceutical composition of this invention. Alphavirus particles comprising this embodiment of recombinant nucleic acid can be produced according to any of the methods of this invention and can be used in any of

5   the methods of eliciting an immune response and/or delivering a NOI to a cell.

As a further embodiment, the present invention provides a recombinant nucleic acid comprising: a promoter that directs transcription of a nucleic acid; an IRES element; and a nucleic acid comprising a coding sequence, wherein the IRES

10   element is operably located such that translation of the coding sequence is via a cap-independent mechanism directed by the IRES element. In this embodiment, transcription of the nucleic acid is uncoupled from translation of the nucleic acid.

It is understood that the foregoing detailed description is given merely by way

15   of illustration and that modifications and variations may be made therein without departing from the spirit and scope of the invention.

EXAMPLES

5   **Example 1.**   Construction of transfer cloning vectors.

A.   EMCV IRES-containing vectors

A transfer vector (pCDNA3.3) was prepared into which the

10   encephalomyocarditis (EMCV) IRES sequence and any NOI could be introduced.
Plasmid pCDNA3.1(+) (Nitrogen) was digested with restriction enzyme Bathe and
treated with T4 DNA polymerase to eliminate the unique Bathe restriction site,
resulting in generation of pCDNA3.2. The pCDNA3.2 DNA was further digested
with restriction enzyme Bay and also treated with T4 DNA polymerase to remove the

15   unique Bay restriction site, resulting in generation of pCDNA3.3.

An intermediate cloning vector containing the multiple cloning site (MCS)
from a VEE replicon vector was prepared by legating an ~ 250bp ApaI/NotI MCS
fragment into ApaI/NotI linearized pBluescript KS+ (Stratagene) DNA, generating

20   pKS-rep2. The EMCV IRES was digested from pD1+2+3 (Kaminski et al., 1995)
with restriction enzymes EcoRI and BamHI and ligated into EcoRI and BamHI
linearized pKS-rep2 DNA, generating pKS-rep2/EMCV. The EMCV IRES and MCS
sequence from the pKS-rep2/EMCV vector were PCR amplified using primers
EMCVF(AscI).2 and EMCVR(AscI).1 (Table 1). The EMCV PCR product was

25   digested with AscI restriction enzyme and ligated into AscI linearized VEE replicon
(pERK) vector DNA, generating pERK/EMCV. To complete the transfer cloning
vector, pERK/EMCV DNA was digested with EcoRV and NotI restriction enzymes
and the 862 bp EcoRV/NotI fragment was ligated into EcoRV and NotI linearized
pCDNA3.3 DNA, generating pCDNA3.3/EMCV. The sequence of the EMCV IRES

30   and associated multiple cloning sites was confirmed in the pCDNA3.3/EMCV vector
before preparing further constructs with it.

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Table 1.

Primer name	5' Primer sequence 3'
EMCVF(AscI).2	TGGCGCGCCGCTCGGAATTCCCCCTCTCCC
EMCVR(AscI).1	AGGCGCGCCTTCTATGTAAGCAGCTTGCC
F'-CAT(BamHI)	GCTGGATCCATGGAGAAAAAATCACTGGA
R'-CAT(XbaI)	CGATCTAGATTACGCCCCGCCCTGCCACTCA
Anti-En(EcoRI)	CGGAATTCATTATCATCGTGTTTTTC
Anti-EN(BamHI)	CGGGATCCCCCCTAACGTTACTGGCCGAAGC
Anti-En(AscI)	AGGCGCGCCATTATCATCGTGTTTTTC
dAvr En(AscI) R	AGGCGCGCCCTAGGGGTCTTTCCCCTCTC
3'UTR4Xbiotin	GCGGCATGCCAATCGCCGCGAGTTCTATGTAAGCAGCTTGCC
GAG-F	CGGGATCCATGGCTGCGAGAGCGTCA
GAG-R	CGGGATCCTTATTGAGACAAGGGGTCGC

B.   XIAP IRES-containing vectors

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The X-linked inhibitor of apoptosis (XIAP) gene 5' noncoding region (NCR) containing the putative IRES element (see Holcik et al. (1999) *Nature Cell Biol* 1: 190-192; Holcik and Korneluk (2000) *Mol Cell Biol* 20:4648-57 and Holcik et al. (2003) *Mol Cell Biol* 23:280-288 for sequence and size of element) was PCR

10   amplified from human fetal liver marathon ready cDNA (Clontech, Palo Alto, CA) using an adaptor primer supplied with the cDNA and an XIAP reverse primer (XIAP-R) followed by a nested PCR using XIAP IRES specific primers. Primers are listed in Table 2. Resulting PCR products of approximately 1007 and 241 bp were TA cloned using a commercially available kit (Invitrogen Corporation; Carlsbad, CA). These

15   constructs possess either 844 nucleotides or 78 nucleotides, respectively, of the XIAP gene noncoding region, in addition to the 163 nucleotide putative XIAP IRES. Sequences for each construct were confirmed by automated DNA sequencing. To generate shuttle vectors for cloning into the VEE replicon, the XIAP sequences were transferred as an EcoRI fragment into the equivalent site of pKS-rep2, generating

20   pKS-rep2/XIAP1007 and pKS-rep2/XIAP241 DNAs.

Table 2

XIAP-R	5'-CCCTGCTCGTGCCAGTGTTGATGC-3'
XIAP/IRES-1007	5'-ACACGTGGGGCAACCCTGATTTATGCCTGTTGTCC-3'
XIAP/IRES-241	5'-AGTTAACTCAAAAGAGAAACAAAAATGC
XIAP/IRES-R	5'-AGATATCTTCTCTTGAAAATAGGACTTGTCCAC-3'
Cap5'F	5'-GTTCCCGTTCCAGCCAATGTATCCG-3'
13-87pr1	5'-GTCACTAGTGACCACCATGT-3'
3-1.1pr1	5'-TAAGAGCCGCGAGCGATCCT-3'

1007 bp XIAP 5'NCR

ACACGTGGGGCAACCCTGATTTATGCCTGTTGTCCCAGTGTGATTATTACT

5   AGTGTAATTTTTCACTTTGAGAAGTGTCCAGGTTTGGAGGATAAATTATCT

TTCTAATAATTGATACCCTTCTCATAACCTAACGGGTTCCTTTTAGTATTTT

ATCTGGGTTAAAATTACCAGCTGTAATTTGGCAGCTCTAATAAGACTGCA

GCAATACTTATCTTCCATTTGAACAGATTGTTACTTGACCAAGGGAAGTTA

ATAGCAAAAGTAACTGCAGGGCACATGTATGTCATGGGCAAAAAAAAA

10   AAGTAACAGCAATTAAGGTTTGCAGGTACTTAGAATTTTTCCTGAGCCACC

CTCTAGAGGGCAGTGTTACATATATATCTGTAATTATCCAGTTACAACAAA

AAAAGGGCTCTCATTCATGCATGAAAATCAGAAATATTTCATACTCTTAA

AGAACACATTGGAACCAATATTATGATTAAAACATATTTTGCTAAGCAAA

GAGATATTAAAAATTAATTCATTAACATTCTGAACATTTTTAACTTGTAA

15   AAACAACTTTGATGCCTTGAATATATAATGATTCATTATAACAATTATGCA

TAGATTTTAATAATCTGCATATTTTATGCTTTCATGTTTTTCCTAATTAATG

ATTTGACATGGTTAATAATTATAATATATTCTGCATCACAGTTACATATT

TATGTAAAATAAGCATTTAAAAATTATTAGTTTTATTCTGCCTGCTTAAAT

ATTACTTTCCTCAAAAGAGAAACAAAAATGCTAGATTTTACTTTATGAC

20   TTGAATGATGTGGTAATGTCGAACTCTAGTATTTAGAATTAGAATGTTTCT

TAGCGGTCGTGTAGTTATTTTATGTCATAAGTGGATAATTTGTTAGCTCC

TATAACAAAGTCTGTTGCTTGTGTTTCACATTTTGGATTTCCTAATATAAT

GTTCTCTTTTAGAAAGGTGGACAAGTCCTATTTTCAAGAGAAGAT

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Example 2. Construction of improved replicon vectors.

A. Constructs containing the EMCV IRES

To demonstrate the functionality of an IRES sequence placed downstream of a functional alphavirus 26S promoter, reporter genes were subcloned into the pCDNA3.3/EMCV transfer vector and then the EMCV/reporter gene cassette was moved into the pERK replicon vector. Initial experiments were conducted using a replicon vector expressing the Chloramphenicol acetyl transferase (CAT) reporter gene. The CAT gene was amplified using primers F'-CAT (BamHI) and R'-CAT (XbaI) (Table 1). The PCR product was digested with BamHI and XbaI restriction enzymes and ligated into BamHI/XbaI linearized pCDNA3.3/EMCV DNA, generating pCDNA3.3/EMCV/CAT. After the sequence of the CAT gene was confirmed, pCDNA3.3/EMCV/CAT DNA was digested with AscI restriction enzyme to release a 1303 bp EMCV/CAT fragment. The AscI digested EMCV/CAT fragment was then ligated into AscI linearized pERK vector DNA, generating pERK/EMCV/CAT.

It has been shown that the EMCV IRES has a directional activity and when it is in the wrong orientation, with regard to a NOI, no cap-independent translation is noted (Roberts and Belsham (1997) *Virology* 227:53-62). In addition, deletion of the 5' terminal sequences of the EMCV IRES abolishes cap-independent translation in the context of a dicistronic expression vector (Van der Velden et al. (1995) *Virology* 214: 82-90; Jang & Wimmer (1990) *Genes & Development* 4:1560-72). To demonstrate that cap-independent translation of the CAT gene is occurring, two pERK vectors identical to pERK/EMCV/CAT were prepared, only with the EMCV IRES in the anti-sense orientation (pERK/anti-EMCV/CAT) or with a 5' deletion of the terminal sequences of the EMCV IRES (pERK/ΔAvr/CAT).

An anti-sense version of the EMCV IRES was PCR amplified from pKS rep2/EMCV DNA using primers anti-En(EcoRI) and anti-En(BamHI) (Table 1). The amplified EMCV IRES fragment was digested with EcoRI and BamHI restriction

enzymes and ligated into EcoRI/BamHI linearized pKS-rep2 DNA, generating pKS-rep2/anti-EMCV. The BamHI/XbaI digested CAT gene described above, was ligated into BamHI/XbaI linearized pKS-rep2/anti-EMCV DNA, generating pKS-rep2/anti-EMCV/CAT. The 1295 bp anti-EMCV/CAT gene cassette was PCR amplified from

5   pKS-rep2/anti-EMCV/CAT DNA using primers EMCVR(AscI).1 and anti-En(AscI) (Table 1). Finally, the anti-EMCV/CAT fragment was digested with AscI restriction enzyme and ligated into AscI linearized pERK vector DNA, generating pERK/anti-EMCV/CAT. The sequence of the anti-EMCV/CAT gene region was confirmed before further experiments were carried out.

10

To generate the ΔAvr/CAT pERK vector, first the ΔAvr deletion was made in the EMCV IRES found in pKS-rep2/EMCV intermediate vector. The deletion was accomplished by digesting pKS-rep2/EMCV DNA with both EcoRI and AvrII restriction enzymes deleting 145 bp from the 5' region of the EMCV IRES. The

15   linearized DNA was treated with T4 DNA polymerase to create blunt ends and religated to generate pKS-rep2/ΔAvr DNA. The CAT gene was cloned into the intermediate vector by ligating the BamHI/XbaI CAT gene described above into BamHI and XbaI restriction enzyme linearized pKS-rep2/ΔAvr, generating pKS-rep2/ΔAvr/CAT DNA. The 1177 bp ΔAvr/CAT gene cassette was PCR amplified

20   from pKS-rep2/ΔAvr/CAT. DNA using primers EMCVR(AscI).1 and dAvr En(AscI) R (Table 1). Finally, the ΔAvr/CAT fragment was digested with AscI restriction enzyme and ligated into AscI linearized pERK vector DNA, generating pERK/ΔAvr/CAT. The sequence of the ΔAvr/CAT gene region was confirmed before further experiments were carried out.

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B. Constructs containing the EV71 IRES

The human enterovirus 71 (EV71) IRES element (Thompson and Sarnow (2003) *Virology* 315: 259-266) was cloned in both sense and antisense orientations

30   into spacer replicon vectors and analyzed for expression of a CAT reporter gene. The EV71 IRES element (strain 7423/MS/87) was PCR amplified from pdc/MS DNA (Thompson and Sarnow, 2003) using primers to produce a sense fragment (dc/MS (EcoRI) F and dc/MS (BamHI) R) and an antisense fragment (dc/anti-MS (EcoRI) R

and dc/anti-MS (BamHI) F) (Table 3). The sense and antisense EV71-MS IRES PCR products were digested with EcoRI and BamHI restriction enzymes and ligated into pCDNA3.3 (see Example 1) linearized with EcoRI and BamHI, generating pCDNA3.3/MS and pCDNA3.3/anti-MS. The EV71-MS IRES regions, in each

5   pCDNA3.3 vectors, were sequenced to verify that no nucleotide changes were introduced during PCR amplification before further experiments were initiated.

The CAT reporter gene, as described above in A., was cloned into BamHI and XbaI linearized pCDNA3.3/MS and pCDNA3.3/anti-MS vectors, generating

10   pCDNA3.3/MS/CAT and pCDNA3.3/anti-MS/CAT, respectively. Spacer replicon constructs were produced by digesting the pCDNA3.3/MS/CAT and pCDNA3.3/anti-MS/CAT DNAs with AscI restriction enzyme and ligating the MS-CAT or anti-MS-CAT AscI fragments into spacer replicon vectors. The spacer-IRES-CAT region of each vector, was sequenced to verify that no nucleotide changes were introduced

15   during cloning before further experiments were initiated.

Table 3

Primer	Sequence 5' – 3'
dc/MS(EcoRI) F	CGAATTCTTAAAACAGCTGTGGGTTG
dc/MS (BamHI) R	CGGGATCCGGTCAACTGTATTGAGGGTTAATATAAAG
dc/anti-MS(BamHI) F	CGGGATCCTTAAAACAGCTGTGGGTTGTTCCCAC
dc/anti-MS(EcoRI) R	GGAATTCGGTCAACTGTATTGAGGGTTAATATAAAG

C. Constructs containing the XIAP IRES

20

The CAT gene was cloned into the EcoRV and BamHI sites of pKS-rep2/XIAP1007 (see Example 4 below) after PCR amplification of the gene using CATF (5'-GGAGAAAAAAATCACTGGATATAC-3') and CATR(Bam) (5'-GGGGATCCTTACGCCCCGCCCTGCCAC-3') primers, generating pKS-

25   rep2/XIAP/CAT 1007. This strategy reconstitutes the wild-type XIAP gene start site. The intermediate was then cloned as an ApaI/SphI fragment into pERK to generate

pERK/XIAP/CAT 1007. Following *in vitro* transcription and electroporation into Vero cells, VRP yields and CAT protein expression in infected cells were determined and compared to pERK/EMCV/CAT 342. VRP yields were equivalent for both constructs. In this particular construct, it has been possible to modify the level of

5   CAT protein expression using the XIAP IRES (3.97 e5 ng/µg) as compared with the EMCV IRES (1.08 e6 ng/µg), thus demonstrating the utility of different IRESs in the claimed invention.

D. Constructs expressing HIVgp160

10   A replicon expressing the HIVgp160 clade C gene was constructed in which translation of the HIVgp160 was directed from the EMCV IRES. In this construct, the 167 bp spacer from the pH1500A/EMCV/Vcap helper construct (see Example 4.B.1.) was cloned into an EMCV IRES replicon construct as follows. The pH1500A/EMCV/Vcap DNA was digested with ApaI restriction enzyme to release a

15   194 bp fragment containing the 167 bp spacer and a portion of the EMCV IRES. A pERK/EMCV 749 vector was also digested with ApaI restriction enzyme and the released 749 bp spacer ApaI fragment was replaced with the 167 bp spacer ApaI fragment, generating the pERK/EMCV 167 vector. To demonstrate that a heterologous gene could also be efficiently expressed and packaged from the

20   pERK/EMCV 167 replicon vector, the HIV clade C gp160 gene (Williamson C et al. (2003) AIDS Res Hum Retroviruses 19:133-44) was cloned into this vector as follows. The HIV gp160 gene was amplified (using primers env-5'-XbaI and DU151gp160 3'-XbaI) (Table 4) and cloned into pCR-XL-TOPO (Invitrogen, Carlsbad, CA), generating pCR-XL-TOPO/gp160. The gp160 gene was sequenced to

25   ensure no errors were introduced during PCR amplification before initiating further studies. The pCR-XL-TOPO/gp160 DNA was digested with XbaI restriction enzyme and the gp160 fragment was then ligated into XbaI linearized pCDNA3.3/EMCV, generating pCDNA3.3/EMCV/gp160. The pCDNA3.3/EMCV/gp160 DNA was digested with AscI restriction enzyme to release the EMCV/gp160 fragment. The

30   EMCV/gp160 fragment was then ligated into AscI linearized pERK/EMCV 167 vector DNA, generating the pERK/EMCV/gp160 167 vector.

Table 4

Primer	Sequence 5'-3'
Env-5'-XbaI	CGACATAGTCTAGACCGCCAAGATGAGAGTGATGG
DU151gp160 3'-XbaI	GATCTCTAGATTATTGCAAAGCTGCTTCAAAGCCC

E.   Construction of double subgenomic IRES replicons expressing multiple NOIs

An IRES replicon vector coding for two 26S-spacer-IRES-NOI cassettes in series was constructed. The base pERK vector used to generate the double subgenomic IRES replicons (pERK MCS2) contained a 342 bp spacer region downstream of the 26S promoter and coded for the following restriction sites in its MCS (5' AscI, SnaBI, SphI 3').

The C-terminal portion of the heavy chain (Hc) of botulinum neurotoxins A and B (BoNT A and BoNT B) was cloned into pCDNA3.3/EMCV as BamHI/XbaI fragments, generating pCDNA3.3/EMCV/BoNT A and pCDNA3.3/EMCV/BoNT B, respectively. The BoNT genes were digested out of the pCDNA3.3/EMCV vectors with AscI restriction enzyme and the AscI EMCV/BoNT cassettes were ligated into AscI linearized pERK MCS2 DNA, generating pERK/BoNT A MCS2 and pERK/BoNT B MCS2 monovalent vectors. Orientation of the insert was determined by restriction analysis and clones with inserts in the sense orientation were isolated. The EMCV IRES and BoNT genes were sequenced to verify that no errors were introduced during cloning before further experiments were initiated.

To generate the double subgenomic BoNT A/B IRES replicon construct (pERK-BoNT A/B MCS2) the monovalent pERK BoNT MCS 2 vectors were utilized. The pERK/BoNT B MCS2 vector was partially digested with PspOM I restriction enzyme and the ends were made blunt using T4 DNA polymerase. The pERK/BoNT B MCS2 DNA was further digested with SphI restriction enzyme to release a 26S-342bp spacer-EMCV-BoNT B fragment. The 26S-342 bp spacer-EMCV-BoNT B fragment was then ligated into SnaBI/SphI digested pERK/BoNT A MCS2 DNA, generating the pERK-BoNT A/B MCS2 vector. The final structure of the construct is 5' NCR-nsP1,2,3,4 – 26S- 342bp spacer-EMCV-BoNT A-26S-342 bp spacer-EMCV-BoNT

B-NCR 3'. The sequence of the double subgenomic IRES replicon was verified before expression and VRP packaging studies were conducted.

F. Construction of an IRES-containing S.A. AR86 replicon

A replicon vector derived from S.A.AR86 (pRep89; described in Heise et al. *J Virol*. 2003 77(2):1149-56) was modified to contain a 342 bp spacer-EMCV-HIV gag cassette downstream of the 26S promoter. The 342bp spacer-EMCV-HIV gag fragment was PCR amplified from pERK/EMCV/gag 342 DNA using primer stuffer 342 (ClaI) and 3-42.pr4 (Table 5). Amplification with the 3-42.pr4 primer allows incorporation of 3' ClaI site that exists just downstream from the HIV gag gene in the pERK/EMCV/gag 342 DNA. The PCR product was then digested with ClaI restriction enzyme and ligated into ClaI linearized pRep89, generating the pRep89/EMCV/gag 342 vector. The entire inserted region was sequenced to ensure that no errors had been introduced during PCR amplification.

Table 5.

Primer	Sequence 5' – 3'
stuffer 342 (ClaI)	CCATCGATCTATTCCAGAAGTAGTGAGG
3-42.pr4	CAATCGCCGCGAGTTCTATG

Example 3. NOI expression analysis from IRES-directed replicons

A. EMCV IRES replicon expression

1.   CAT Expression

CAT protein expression was examined using the pERK/EMCV/CAT, pERK/anti-EMCV/CAT, and pERK/ΔAvr/CAT replicon constructs. Capped replicon RNAs were *in vitro* transcribed using a T7 RiboMax kit (Promega Corporation; Madison, WI; Cat No. P1300). RNAs were purified using RNeasy purification columns (Qiagen Corporation, Germantown, MD) following the manufacturers instructions. Vero cells (6 x 10^6 cells) suspended in 0.4 ml InVitrus™ chemically defined cell culture medium, (Cell Culture Technologies GmbH, Zurich, CH; Catalog No. IVT) and electroporated with 15 µg of either pERK/EMCV/CAT or pERK/anti-

EMCV/CAT RNA using a Bio Rad Gene Pulser (BioRad Laboratories, Hercules, CA). Cells were pulsed four times with the electroporator set at 290 volts and 25 microfarads. CAT expression was detected by IFA using a rabbit anti-CAT antibody on methanol fixed cells and by ELISA using electroporated cell lysates and a

5   commercially available CAT ELISA kit (Boehringer Mannheim, Indianapolis, IN).

Random DNA fragments were cloned between the EMCV IRES sequence and the VEE subgenomic promoter at a unique EcoRV site located in the pERK vectors. The small DNA fragments cloned between the 26S promoter and the EMCV IRES

10   came from AluI restriction enzyme digested pCDNA3.1(-) DNA. The AluI restriction enzyme cuts frequently within pCDNA3.1(-) DNA resulting in blunt end fragments ranging in size from 706 bp to 6 bp. The AluI digested pCDNA3.1(-) fragments were ligated into EcoRV linearized pERK/EMCV/CAT, pERK/anti-EMCV/CAT, and pERK/ΔAvr/CAT DNAs. Individual clones were sequenced to determine what spacer

15   fragment had been cloned into each new vector. The size of some of the spacer fragments found in the vectors was larger than the largest predicted pCDNA3.1(-) AluI fragment, due to ligation of multiple fragments into the spacer region of these replicons. Each spacer-IRES replicon was transcribed and the RNA electroporated into Vero cells as described above. CAT protein expression was monitored by CAT

20   ELISA and the results are summarized in Table 6.

Table 6. CAT expression analysis from EMCV-IRES containing replicons

Replicon	size of spacer fragment	ng CAT/μg total protein
pERK/anti-EMCV/CAT	133	2.1
pERK/EMCV/CAT	234	9.9
pERK/anti-EMCV/CAT	234	1.5
pERK/ΔAvr/CAT	234	0.4
pERK/ΔAvr/CAT	226	0.5
pERK/EMCV/CAT	342	10.3
pERK/anti-EMCV/CAT	357	0.1
pERK/EMCV/CAT	805	7.4
pERK/anti-EMCV/CAT	706	0.5
pERK/ΔAvr/CAT	681	0.02

The results indicate that CAT expression from pERK/IRES/CAT replicon constructs containing spacer fragments is robust and directed by the IRES, as compared with similar vectors with no spacer fragments (approximately 4-7 ng

5   CAT/µg total protein). The highest levels of expression of the heterologous gene occurred when spacer fragments greater than approximately 200 nucleotides were introduced between the 26S promoter and the EMCV IRES sequences.

2.   Multiple NOI expression from a single replicon

10

Expression and packaging of the pERK-BoNT A/B MCS2 replicon were carried out in Vero cells. Capped pERK-BoNT A/B replicon RNA was transcribed and purified as described above. Vero cells (1×10^8 cells) were electroporated with 30 µg of replicon RNA, 30 µg of capsid helper RNA and 30 µg of glycoprotein helper RNA.

15   Electroporated cells were analyzed by IFA using horse anti-BoNT A and BoNT B antibodies (Perimmune, Rockville, MD) before VRP were harvested. Results of the IFA and titration of VRP generated are shown in Table 7.

Table 7

Replicon	Anti-BoNT A IFA	Anti-BoNT B IFA	VRP titer
pERK-BoNT A/B MCS2	Positive	Positive	2×10^9 VRP

20

3.   HIV gp160 Expression

The pERK/EMCV/gp160 167 replicon (Example 2D) was analyzed for expression of the gp160 gene and VRP generation. Purified RNA was prepared for

25   the replicon, GP helper and capsid helper as described above. Vero cells were electroporated with the RNAs and VRP were collected 20 – 24 hours post electroporation. Results of IFA and VRP titration are summarized in Table 8. For comparison, a pERK replicon expressing gp160 directly from the 26S promoter was also evaluated.

30

44

Table 8.

Replicon	Anti-gp160 IFA	VRP titer/ml
pERK/gp160	Positive	2.1×10^8
pERK/EMCV/gp160 167	Positive	2.5×10^8

4.   HIV GAG expression from a S.A. AR86 Replicon

5   pRep89/EMCV/gag 342 DNA was transcribed *in vitro*, using an SP6 RiboMax

kit (Promega Corporation; Madison, WI; Cat No. P1280), to generate capped replicon

RNA. RNA was purified using RNeasy purification columns (Qiagen Corporation,

Germantown, MD) following the manufacturers' instructions. Vero cells (1×10^8

cells) were electroporated with 30 ug of Rep89/EMCV/gag 342 RNA and then

10   analyzed for Gag protein expression ~ 18 hr post electroporation. Anti-Gag IFA

analysis of Rep89/EMCV/gag 342 electroporated cells was positive for Gag protein

expression

B. EV71-MS IRES replicon expression

15

Expression of CAT protein from each EV71-MS containing replicon was carried

out in Vero cells. Capped replicon RNA was transcribed and purified as described

above. Vero cells ($2\text{-}3 \times 10^7$ cells) were electroporated with 30 μg of replicon RNA.

Electroporated cells were analyzed by IFA using anti-CAT (Cortex Biochem, San

20   Leandro, CA) and anti-VEE nsp2 antibodies (AlphaVax) approximately 18 hours post

electroporation. In addition, CAT expression was monitored by ELISA as described

above. Results of IFA and CAT ELISA comparing activity detected from

pERK/EMCV/CAT 342 and pERK/MS/CAT 342 replicons are shown in Table 9.

25   Table 9.

Replicon	Anti CAT IFA	Anti VEE nsp2 IFA	ng CAT/μg protein	% reduction in translation
pERK/MS/CAT 342	+	+	20.1	NA
pERK/anti-MS/CAT 342	-	+	0.6	97%

45

pERK/EMCV/CAT 342	+	+	14.8	NA
pERK/ΔAvr/CAT 342	-	+	0.0	>99%

Example 4. IRES-directed translation with different spacers

A.   Replicon Constructs

1.   EMCV IRES-containing constructs

Pairs of replicon constructs coding for either the EMCV or antisense-EMCV IRES sequences were prepared that contained exactly the same spacer region. These comparisons demonstrate that only the EMCV IRES sequences in the sense-orientation (i.e. in the 5'-3' orientation in which the sequence is found in the virus) direct cap-independent translation; that is, very little translation occurs when the IRES is in an anti-sense orientation, indicating that a properly-oriented IRES element is required to obtain significant CAT expression in these constructs. These replicon constructs were prepared as described above. Each spacer-IRES replicon was *in vitro* transcribed and 30 µg of each purified RNA was electroporated into ~ 1 x 10^7 Vero cells as described above. CAT protein expression was monitored by CAT ELISA and the results are summarized in Table 10.

Table 10. Comparison of CAT expression using spacer-EMCV or spacer-anti-EMCV IRES replicons.

replicon	size of spacer fragment	ng CAT/ µg total protein	replicon	size of spacer fragment	ng CAT/ µg total protein	% reduction in translation*	Fold increase in translation[#]
EMCV/CAT	257	16.9	Anti-EMCV/CAT	257	3.1	82.7	5.5
EMCV/CAT	342	35.6	Anti-EMCV/CAT	342	0.2	99.4	178
EMCV/CAT	357	7.6	Anti-EMCV/CAT	357	0.4	94.7	19
EMCV/CAT	383	28.7	Anti-	383	0.6	97.9	48

46

			EMCV/CAT				
EMCV/CAT	579	40.0	Anti-EMCV/CAT	579	0.3	99.2	133
EMCV/CAT	749	6.74	Anti-EMCV/CAT	749	0.03	99.5	224

*% reduction in translation in the anti-sense oriented IRES constructs relative to the sense-oriented, IRES directed constructs

#Fold increase in translation from the sense oriented IRES element relative to translation from constructs with an anti-sense oriented IRES element

The data show that CAT protein expression was greatly reduced (in most cases, >95%) when the replicon contained a spacer and an anti-sense EMCV IRES upstream of the CAT gene. Furthermore, the data demonstrate the capability of an IRES-directed protein expression system to optimize the level of expression of NOI. The optimization is NOI-specific, but utilizing the teachings herein, the identification of spacer-IRES combinations that provide the desired level of expression for any given NOI would be routine to one of ordinary skill in the art.

2. Use of a spacer derived from a 5' non-coding region

A pERK replicon was engineered to contain the full-length VEE capsid protein gene by PCR amplifying the capsid sequence from pH500A/Vcap using the Cap5'F and 3-1.1pr1 primers (Table 11). The resulting PCR product was inserted into the EcoRV and SphI restriction enzyme sites of pERK. "pERK/Capsid," was modified further to contain a unique AscI restriction enzyme at the 3' end of the capsid gene using AscIF and AscIR primers (Table 11) for site-directed mutagenesis using a commercially available kit (Stratagene). Serial truncations of the VEE capsid sequence were then generated by PCR amplification of sequences from pERK/Capsid using a forward primer (13-82.2.16) that anneals within the nsP4 gene and reverse primers (Table 11), that have been engineered to contain an AscI restriction enzyme site. PCR products were digested with ApaI and AscI or SwaI and AscI and cloned back into pERK/Capsid to generate pERK/Cap200, pERK/Cap400 and pERK/Cap600. These replicons retain increasing amounts of sequence from the 5' end of the capsid gene to function as a "spacer" between the 26S promoter and the downstream constructs to be inserted. To introduce an EMCV/CAT cassette into each of the pERK/Cap vectors described above, pCDNA3.3/EMCV/CAT DNA was

digested with AscI restriction enzyme to release a 1303 bp EMCV/CAT fragment.
The AscI digested EMCV/CAT fragment was then ligated into the AscI linearized
pERK/Cap vector DNAs, generating pERK/EMCV/CAT Cap 200,
pERK/EMCV/CAT Cap 400 and pERK/EMCV/CAT Cap600.

5

Table 11: Primers for generating capsid spacer replicons.

Cap5'F	5'-GTTCCCGTTCCAGCCAATGTATCCG-3'
3-1.1pr1	5'-TAAGAGCCGCGAGCGATCCT-3'
AscIF	5'-CCGCGAGTTCTATGTAAGCGGCGCGCCAATTGTTAC AGACACATGGTGG-3'
AscIR	5'-CCACCATGTGTCTGTAACAATTGGCGCGCCGCTTACA TAGAACTCGCGG-3'
13-82.2.16	5'-GCTCTTTTTGCGAAGACACATAAT-3'
CAP200(AscI)	5'- TTGGCGCGCCTTCTTCGGTTTCTTAGCGGATGGCCC-3'
CAP400(AscI)	5'- TTGGCGCGCCCTTCCAACATGATTGGGAACG-3'
CAP600(AscI)	5'- TTGGCGCGCCTGTAATAGCCTTGGGGTTTCTCATGGG-3'

These replicons, containing portions of the 5' region of the VEE capsid gene,
were linearized, *in vitro* transcribed, electroporated into Vero cells and analyzed for
10   CAT protein expression by IFA and ELISA. CAT protein expression was verified by
IFA using CAT-specific antibodies; however, the intensity of immunofluorescence
varied depending on the length of the capsid gene spacer used. These results were
reflected in the CAT ELISA (Table 12).

15   Table 12: Cat protein expression from replicons containing capsid gene spacers

Construct	CAT IFA	nsP2 IFA	CAT Protein
pERK/EMCV/CAT Cap 200	75%	95%	29 ng/µg total prot.
pERK/EMCV/CAT Cap 400	60%	95%	2 ng/µg total prot
pERK/EMCV/CAT Cap 600	60%	95%	5 ng/µg total prot.
pERK/EMCV/CAT 342	50%	50%	14 ng/µg total prot.

B. Helper Constructs

1.   Constructs comprising the EMCV IRES

5   Helpers were constructed which individually expressed either the VEE glycoprotein genes ("GP") or the VEE capsid gene. Initially, two empty helper backbone vectors were generated to facilitate construction of spacer-IRES containing capsid and GP helpers. One empty helper was generated by digesting the pERK vector with ApaI and RsrII restriction enzymes to remove 6989 bp of the

10   nonstructural protein coding region. The DNA was treated with T4 DNA polymerase to produce blunt ends before ligating the nonstructural gene-deleted pERK vector to produce pH500G. The pH500G empty helper contained approximately 500 nucleotides of the 5' noncoding region (NCR). The second empty helper was generated by digesting the pERK vector with SwaI and RsrII restriction enzymes to

15   remove 6449 bp of the nonstructural protein coding region. The DNA was treated with T4 DNA polymerase to produce blunt ends before ligating the DNA, generating pH1500G. The pH1500G empty helper contained approximately 1500 nucleotides of the 5' NCR, including an additional 540 bp of the nsp4 gene immediately upstream of the 26S promoter that is not present in the pH500G helper. Empty helper constructs

20   were also prepared that coded for an A rather than a G residue at nucleotide 3 (pH500A and pH1500A). These constructs were prepared by subcloning the 5' NCR region from a capsid helper (pH500A/Vcap), which contains an A at nucleotide 3, in place of the same region in pH500G and pH1500G. This was accomplished by digesting pH500A/Vcap with XbaI and SacI restriction enzymes, collecting the 430

25   bp fragment and ligating it into XbaI and SacI digested pH500G and pH1500G DNAs, generating pH500A and pH1500A respectively.

The capsid and GP genes were cloned into pCDNA3.3/EMCV and pKS-rep2/anti-EMCV as BamHI and XbaI fragments as described above. The

30   EMCV/capsid, anti-EMCV/capsid, EMCV/GP and anti-EMCV/GP cassettes were cloned into the pH500G, pH500A, pH1500G and pH1500A empty helper constructs as AscI fragments as described above. The sequence of each helper was confirmed before further experiments were initiated.

Random spacer fragments were cloned between the 26S promoter and the EMCV or anti-EMCV IRES in each helper at a unique EcoRV site as previously described. The sequence and length of the inserted spacer fragments was determined for each new helper, and the length of the spacer insert is included at the end of the construct designation. Spacers #15, 16, and 22 were not further characterized. The constructs pH500A/EMCV/GP and pH500A/anti-EMCV/GP contain no spacer.

2.   Packaging and Titers using EMCV IRES-containing GP and/or Capsid Helper Combinations

Various combinations of the GP and Capsid helpers were used to package a VEE replicon expressing the HIV-GAG protein, pERK-342/EMCV/*gag* (see Example 7 for a description of the construction of this replicon). For the results presented in Table 13, 30 µg of each RNA helper and 30 µg of the replicon RNA were co-electroporated into Vero cells in a 0.8 ml electroporation cuvette, using 4 pulses at 580 V and 25 µF, and the cells were allowed to recover at room temperature for 10 min. Electroporated cells were seeded into T-175 flasks containing 50 ml EMEM (10% FBS) with antibiotics and incubated at 37°C. After 20-24 hours, VEE replicon particles ("VRPs") were collected and tittered on Vero cells in 96-well plates by measuring GAG protein expression using an immunofluorescence assay (IFA). The VRP yield (Table 13) from each electroporation is expressed on an "IU/ml" basis, for comparative purposes.

Table 13.

Capsid Helper	GP Helper	Yield of VRPs (IU/ml)
pH500A/EMCV/Vcap 384	pH500A/EMCV/GP 393	1.6 e6
pH500A/EMCV/Vcap 291	pH500A/EMCV/GP 393	1.32 e6
pH1500A/EMCV/Vcap 167	pH500A/EMCV/GP 393	1.51 e6
pH500A/Vcap	pH500A/EMCV/GP 393	1.92 e5
pH500A/Vcap	pH500A/EMCV/GP #15	2.35 e5
pH500A/Vcap	pH500A/EMCV/GP #16	5.55 e5
pH500A/Vcap	pH500A/EMCV/GP #22	1.15 e6

pH500A/EMCV/Vcap 291	pH500A/EMCV/GP 291	2.22 e6
pH1500A/EMCV/Vcap 167	pH500A/EMCV/GP 291	5.16 e6
pH500A/Vcap	pH500A/EMCV/GP 291	1.75 e5
pH500A/EMCV/Vcap 291	pH500A/EMCV/GP	1.00 e7
pH1500A/EMCV/Vcap 167	pH500A/EMCV/GP	6.20 e7
pH500A/EMCV/Vcap 384	pH500A/EMCV/GP 376	2.99 e5
pH500A/EMCV/Vcap 291	pH500A/EMCV/GP 376	1.49 e5
pH1500A/EMCV/Vcap 167	pH500A/EMCV/GP 376	1.71 e5
pH500A/Vcap	pH500A/EMCV/GP 376	8.53 e4
pH500A/EMCV/Vcap 384	pH500A/EMCV/GP 342	8.11 e5
pH500A/EMCV/Vcap 291	pH500A/EMCV/GP 342	8.32 e5
pH1500A/EMCV/Vcap 167	pH500A/EMCV/GP 342	1.07 e6
pH500A/Vcap	pH500A/EMCV/GP 342	1.92 e5
pH500A/EMCV/Vcap 291	pH500A/GP	3.56 e8 1.00 e8
pH1500A/EMCV/Vcap 167	pH500A/GP	1.13 e8 2.37 e7

In other experiments, the amount of GP Helper RNA was varied in the electroporation milieu; all other conditions for VRP production were as described above. The results are shown in Table 14.

Table 14.

Capsid Helper	GP Helper	μg GP RNA	VRP Yield (IU/ml)
pH500A/Vcap	pH500A/EMCV/GP 393	45	1.51 e6
pH500A/Vcap	pH500A/EMCV/GP 393	60	2.24 e6

3.   26S-IRES GP Helpers without a Spacer

This experiment was performed to see whether a spacer was required in the GP Helper to uncouple transcription from translation. Vero cells were separately electroporated with each of the following mixtures:

5   a.   Gag Replicon Vector (see Ex. 6) + pH500A/anti-EMCV/GP + pH500A/anti-EMCV/Vcap 291

       b.   Gag Replicon Vector + pH500A/EMCV/GP + pH500A/EMCV/Vcap 291

Cells were incubated as described previously to allow VRP production and the

10   VRPs were harvested and tittered on VERO cells by IFA. In the case of the helpers with the IRES in the sense orientation (the "b." mix), the VRP yield was 3.3 e6; while in the case of the helpers in which the IRES is placed in the anti-sense orientation, the VRP yield was 5.3 e2.

15   4. Production and Use of VEE helper constructs containing the XIAP IRES

The VEE capsid ("VCap") and glycoprotein ("VGP") genes were PCR amplified from pH500A/Vcap and pH500A/GP, respectively, using PFU pol (Stratagene; LaJolla, CA) and Cap5'F or 13-87pr1 forward primers and 3-1.1pr1

20   reverse primers (Table 2, see Example 1B). The resulting PCR products were cloned into the EcoRV and SphI sites of pKS-rep2. This strategy reconstitutes the VEE structural protein start codon at the wild-type start of the XIAP gene. The VEE structural protein sequence in each plasmid was verified by automated DNA sequencing, and the resulting plasmids were used for *in vitro* transcription. RNA was

25   purified using Qiagen RNeasy columns and electroporated into Vero cells for analysis of protein expression and packaging. All helpers expressed either VEE capsid or glycoproteins as determined by IFA, and titers recovered for a VEE replicon expressing the HIV GAG protein ranged from 1×10^5 to 1×10^7 total.

30   The XIAP1007-VEE structural protein construct described above was also cloned into a second helper plasmid, pH1500A, as an ApaI/SphI DNA fragment, generating pH1500A/XIAP/Vcap 1007 and pH1500A/XIAP/GP 1007. These plasmids were used to make RNA and electroporated into Vero cells as above to analyze protein expression and VRP packaging. Again, the resulting helpers

expressed either the VEE capsid or glycoprotein as determined by IFA, and titers ranged from 1×10^8 to over 1×10^9 total VRP, demonstrating the gain from the transcription of the subgenomic mRNA from the 26S promoter.

5   **Example 5.**

Northern analysis was carried out on total cellular RNA collected from Vero cells into which replicon RNAs were electroporated. Spacer-IRES replicon constructs were *in vitro* transcribed and 30 µg of RNeasy column-purified RNA was

10   electroporated into approximately 1×10^7 Vero cells, as described above. The electroporated cells were resuspended in 10 ml of DMEM media, then 7 ml (approximately 7×10^6 cells) were seeded into one 25 cm^2 flask. Total cellular RNA was collected from the cells16 hr post electroporation using an RNAwiz extraction kit (Ambion) following the manufacturers' instructions. The RNAs were quantified and

15   10 µg of each were run on a 1% glyoxal agarose gel before being transferred to a Brightstar-Plus membrane (Ambion) by passive transfer. The RNAs were UV crosslinked to the membrane, blocked with UltraHyb (Ambion) solution for 1 hr at 45°C, and probed overnight with UltraHyb solution containing a biotinylated anti-sense primer (3' UTR4Xbiotin, Table 1) specific for the 3' UTR of the VEE

20   subgenomic RNA (Integrated DNA Technologies, Coralville, IA) 45°C. After overnight hybridization the blot was processed by chemiluminescent RNA detection using a Brightstar Biodetect kit (Ambion) following the manufacturers instructions and visualization with a Epi Chemi II Darkroom (UVP, Inc., Upland, CA). Results of Northern analysis of RNA from Vero cells electroporated with pERK/EMCV/CAT

25   257, pERK/anti-EMCV/CAT 257, pERK/EMCV/CAT 579, or pERK/anti-EMCV/CAT 579 is shown in Figure 1. Both the EMCV and anti-EMCV replicon constructs produced subgenomic transcripts of nearly equal intensity, indicating that the lack of expression of CAT protein from spacer-anti-EMCV/CAT replicon constructs was not due to any substantive reduction in subgenomic RNAs.

30

Example 6. Construction of an HIV$_{gag}$ gene IRES-directed replicon vector

      An HIV subtype C gag gene was cloned into the pERK/EMCV vector containing a 342 bp spacer (pERK-342), as described above. The gag gene was PCR

5   amplified from pERK/HIV$_{gag}$ DNA using primers GAG-F and GAG-R (Table 1). The primers were engineered to contain BamHI restriction sites such that the PCR product would code for this site at the 5' and 3' ends. The PCR product was digested with BamHI restriction enzyme and ligated into BamHI linearized pCDNA3.3/EMCV DNA. Orientation of the gag gene was determined by restriction analysis and a

10   construct with the gene in the correct orientation was selected, generating pCDNA3.3/EMCV/gag. The EMCV/gag gene cassette was digested from pCDNA3.3/EMCV/gag DNA with AscI restriction enzyme and ligated into AscI linearized pERK-342 DNA. Orientation of the EMCV/gag gene cassette was determined by restriction analysis and a construct with the gene in the correct

15   orientation was selected, generating pERK-342/EMCV/gag. The sequence of the EMCV/gag region was verified before further experiments were initiated.

      Analysis of gag protein expression, by IFA and Western blot, indicated that the protein expressed under the direction of the IRES in the pERK-342/EMCV/gag

20   replicon is indistinguishable from the protein expressed from a pERK/HIV$_{gag}$ replicon in which both translation and transcription are directed by the 26S VEE subgenomic promoter. In addition, the level of expression , as measured by titering VRP, was increased with the IRES-directed system as compared to the 26S promoter-directed system (Table 15).

25

Table 15. Comparison of VRP titers generated with different replicon vectors

Replicon vector	VRP titer
pERK/HIV$_{gag}$	4.0×10^8 IFU
pERK-342/EMCV/gag	5.3×10^8 IFU

Example 7. Humoral and cellular immune responses in mice inoculated with IRES-directed HIV gag replicon particles.

The pERK/EMCV/gag 342 replicon elicits robust humoral and cellular
responses when vaccinated into animals. Four-to-five week-old female BALB/c mice
were obtained from Charles River and were acclimatized for one week prior to any
procedure. For the prime and boost, groups of mice were inoculated in both rear
footpads under isofluorane anesthesia with a target dose of 5×10^5 IFU of VRP in
diluent containing PBS with 1% v/v human serum albumin and 5% w/v sucrose.
Footpad injections were performed with a 30.5 G needle and a 0.100 mL Hamilton
syringe by injecting 20 µL in each hind footpad. Serum samples were obtained by
retro-orbital bleeding under isofluorane anesthesia before the first inoculation on Day
0 (pre-bleed), Day 21 (20 days after the primary inoculation) and Day 29 (7 days after
the boost). The vaccination schedule is summarized in Table 16. Spleens were
harvested 14 days after boost for IFN-γ ELISPOT assays

Table 16. IRES-directed replicon VRP vaccination schedule

Group	N	Mouse strain	VRP Vaccine	Dose, IFU	Route	Inoculation Day	Serum Sampling Day
1	5	BALB/c	EMCV/Gag 342[2]	5×10^5	sc-fp[4]	Day 1 & 22	Day 0, 21, 29
2	5	BALB/c	EMCV/Gag 342[2]	5×10^5	sc-fp[4]	Day 1 & 22	Day 0, 21, 29
3	5	BALB/c	Control VRP[3]	5×10^5	sc-fp[4]	Day 1 & 22	Day 0, 21, 29

1: GMP manufactured Gag VRP prepared with un-modified pERK replicon vector
2: 342 refers to the number of nucleotides in the spacer upstream of the IRES/Gag cassette.
3: Control VRP consist of replicons expressing an HIV Pol/Nef gene.
4: sc-fp refers to subcutaneous footpad.

A. Immunologic assays performed after vaccination

Gag ELISA: Purified recombinant histidine-tagged (his)-p55 from HIV-1
subtype C isolate DU-422 was used as antigen coat. Sera were evaluated for the
presence of Gag-specific antibodies by a standard indirect ELISA.

Gag ELISPOT Assay : Viable lymphocytes harvested from spleens were
seeded into individual ELISPOTassay wells in a Multiscreen Immobilon-P ELISPOT

plate (ELISPOT certified 96-well filtration plate, Millipore, Bedford, MA) that had been pre-coated with an anti- IFN-γ monoclonal antibody AN18 (rat IgG1, MabTech, Mariemont, OH), and incubated for 16-20 hours. Cells were removed by multiple washes with buffer and the wells were incubated with a biotinylated anti-

5   IFN-γ monoclonal antibody R4-6A2 (rat IgG1, MabTech), followed by washing and incubation with Avidin-Peroxidase-Complex (Vectastain ABC Peroxidase Kit, Vector Laboratories, Burlingame, CA). To allow for the complex to form, the Avidin-Peroxidase Complex was prepared at least 30 minutes before completion of the incubation period with the secondary antibody and was stored at room temperature.

10   Following incubation, the wells were washed and incubated for 4 minutes at room temperature with substrate (AEC tablets, Sigma) to facilitate formation of spots, which represent the positions of the individual IFN-γ -secreting cells during culture. Spot development was stopped by distilled water rinse.

15   To enumerate Gag-specific IFN-γ secreting cells in lymphocytes from mice immunized with HIV$_{gag}$ VRP, lymphocytes were stimulated with the immunodominant CD8+ CTL H-2K^d-restricted HIV-Gag peptide AMQMLKETI or an irrelevant HA (influenza hemagglutinin) CD8+ CTL H-2K^d-restricted peptide IYSTVASSL that binds to MHC Class I, for 16-20 hours (5% CO_2 at 37°C). Cells

20   minus peptide serve as a background control. As a positive control, cells were stimulated with 4 µg/mL Conconavalin A for a similar time period. Peptides were synthesized with free ends and purified to >90% by New England Peptide.

    HIV$_{gag}$VRP Potency Titration: A Gag-specific IFA of HIV$_{gag}$VRP infected

25   Vero cells was used to measure the potency or infectious titer of the vaccines. Potency is measured as infectious units per mL, IFU/mL. On the day of each injection residual inocula were back-titrated to determine the actual dose each animal received (Table 17).

30

Table 17. Summary of Gag ELISA and ELISPOT results

Mouse #	HIV VRP Vaccine	Inoculations Dose (IFU)		Gag Ab Titers			ELISPOT[1] (SFC/1e6 lymphocytes)
		Prime Day 1	Boost Day 22	Pre-bleed Day -1	7 Days Post Boost Day 29	GMT[2]	14 Days Post Boost Day 36
1-1	EMCV/gag 342	6.8e5	4.4e5	<40	20480		
1-2				<40	40960		341
1-3				<40	20480		
1-4				<40	20480		
1-5				<40	20480	23525	323
2-1	EMCV/gag 342	1.2e6	5.6e5	<40	5120		
2-2				<40	10240		438
2-3				<40	10240		
2-4				<40	20480		
2-5				<40	40960	13512	741
3-1	control VRP	2.8e5	2.2e5	<40	<40		
3-2				<40	<40		7
3-3				<40	<40		
3-4				<40	≥ 40 (OD=0.32)		
3-5				<40	≥ 40 (OD=0.32)		46

1: SFC/1e6 lymphocytes refers to spot forming cells per 1×10^6 lymphocytes
2: GMT, geometric mean titer

Results of the vaccination study indicate that the 342/EMCV/*gag* VRP vaccinated animals mounted a robust humoral and cellular immune response to HIV-Gag, as measured by anti-Gag antibody ELISA and Gag specific ELISPOT assays.

Example 8.

The activity of several insect virus IRES sequences was compared to the activity of a mammalian-virus IRES (EMCV) in a number of insect cell lines. Replicon vectors were designed such that the 26S subgenomic transcript would be bi-cistronic. The 26S subgenomic RNA is capped, meaning that translation of the first gene on the bi-cistronic RNA (Chloramphenicol acetyl transferase (CAT)) is cap-dependent while translation of the second gene (luciferase (LUC)) is dependent on the IRES sequence (cap-independent). Sindbis virus-based replicon vectors were engineered to contain the following elements: 5'NCR, nsp1,2,3,4, 26S promoter, CAT gene, IRES, LUC

gene, NCR 3'. Two insect virus IRES sequences, one derived from *Acyrthosiphon pisum* virus (APV) and the other from *Rhopalosiphum padi* virus (RhPV), were engineered between the CAT and LUC genes. For comparison, a mammalian virus IRES (EMCV) was engineered between the CAT and LUC genes into the same

5   Sindbis replicon vector. RNA for each replicon construct and an RNA helper that coded for all of the Sindbis structural protein genes (capsid-E3-E2-6K-E1) were transcribed *in vitro* using SP6 RNA polymerase. Sindbis replicon particles were prepared by electroporating helper RNA and each of the bi-cistronic replicon RNAs into 8×10^6 BHK-21 cells. The media was collected, clarified, and replicon particles

10   were purified by centrifugation through a 20% sucrose cushion (24,000 RPM for 3 hr at 4°C). Replicon particles were titrated using a rabbit anti-CAT antibody (Cortex Biochem, San Leandro, CA).

To determine the activity of the insect virus IRES sequences in comparison to

15   the EMCV IRES, the purified Sindbis replicon bi-cistronic particles were used to infect a number of different insect cells growing in culture. Insect cells used in these experiments were: *Toxorhynchites amboinensis*, *Anopheles albimanus*, *Anopheles gambiae*, and *Aedes albopictus*. Insect cells were infected at an MOI of 0.1 with replicon bi-cistronic particles. Approximately 16 hr post infection cell lysates were

20   prepared and the amount of CAT protein present in the lysates was determined using a CAT ELISA kit (Roche, Indianapolis IN) following the manufacturers instructions. In parallel, the amount of LUC protein present in the lysates was determined using a luciferase assay kit (Roche). The amount of CAT and LUC detected in each lysate was normalized for the quantity of protein used in each assay to allow comparison of

25   the two values (Table 17). The CAT protein detected in each cell type was similar regardless of the replicon used. This data indicates that similar infection efficiencies were attained within a cell type for each of the three IRES containing replicon particles, and thus the LUC activity detected in each cell type directly reflects the activity of the IRES sequence in that cell type. In each of the insect cell types

30   analyzed, the insect-virus IRES had more activity (85-95% more) than the EMCV IRES (Table 17).

Table 17. Comparison of insect-virus IRES (APV or RhPV) activity and mammalian-virus IRES (EMCV) activity in different insect cell types.

Insect cell type	IRES analyzed	ng CAT/ μg protein	LUC activity (RLU)/μg protein	% difference from EMCV
Tox. amboinensis	APV	2.0	290.5	88%
Tox. amboinensis	RhPV	2.1	231.4	85%
Tox. amboinensis	EMCV	1.6	33.1	0%
An. Albimanus	APV	2.9	497.7	93%
An. Albimanus	RhPV	2.0	468.6	93%
An. Albimanus	EMCV	2.3	31.8	0%
An. gambiae	APV	1.8	525.7	95%
An. gambiae	RhPV	1.7	283.6	91%
An. gambiae	EMCV	1.8	24.2	0%
Ae. albopictus	APV	4.8	87.3	93%
Ae. albopictus	RhPV	4.1	119	95%
Ae. albopictus	EMCV	4.7	5.7	0%

Example 9. Humoral and cellular immune responses to an IRES replicon in primates

A study on the immunogenicity of the pERK/EMCV/gag 342 containing VRPs (Example 6) was also conducted in cynomolgus macaques at the Southern Research Institute in Frederick, MD. Each vaccine was administered to six animals by subcutaneous and intramuscular injection (three animals/route). Animals received two inoculations of 1 x 10^8 vaccine particles at 0 and 1 month. Humoral immune responses were analyzed 4-weeks after the second inoculation (as described in Example7A), and are presented in Table 18. For comparison, a VEE replicon expressing the gag protein directly from the 26S promoter (pERK/gag) was also evaluated.

Table 18.

Construct	Route	ELISA GMT
pERK/EMCV/gag 342	Subcutaneous	1613
pERK/EMCV/gag 342	Intramuscular	640
pERK/gag	Subcutaneous	403
pERK/gag	Intramuscular	1280

Although the present process has been described with reference to specific details of certain embodiments thereof, it is not intended that such details should be regarded as limitations upon the scope of the invention except as and to the extent that

5   they are included in the accompanying claims.

Throughout this application, various patents, patent publication, journal publications and other publications are referenced. The disclosures of these publications in their entireties are incorporated by reference into this application in

10   order to more fully describe the state of the art to which this invention pertains and to provide written description for the subject matter of the sentence in which these references appear in this application.